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From: Ibrahim, Medina A.  
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OM nucleic - nucleic search, using sw model  
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Title: US-09-771-045A-35  
Perfect score: 1299  
Sequence: 1 atggcacttgaccagagcta.....gcttggtgccgcagcatag 1299

Scoring table: IDENTITY NUC  
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DEFINITION Sequence 37 from patent US 6211434.  
ACCESSION AR145465  
VERSION AR145465.1 GI:15107332  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1929)  
AUTHORS Duwick,J.P., Gilliam,J.T. and Maddox,J.R.  
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides  
and methods of use  
JOURNAL Patent: US 6211434-A 37 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..1929  
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BASE COUNT 451 a 539 c 532 g 407 t  
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Query Match 99.8%; Score 1925.8; DB 6; Length 1929;  
Best Local Similarity 99.9%; Pred. No. 0;  
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QY 1861 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAGAGTTGTGCTAGCCTGGTGCCA 1920  
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Db 1861 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAGAGTTGTGCTAGCCTGGTGCCA 1920  
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Db 1921 GCAGCATAG 1929  
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RESULT 3  
AR145466  
LOCUS AR145466 1930 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 39 from patent US 6211434.  
ACCESSION AR145466  
VERSION AR145466.1 GI:15107333  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1930)  
AUTHORS DuVick,J.P., Gilliam,J.T. and Maddox,J.R.  
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides  
and methods of use  
JOURNAL Patent: US 6211434-A 39 03-APR-2001;  
FEATURES Location/Qualifiers  
#source 1..1930  
BASE COUNT 449 a 531 c 537 g 412 t 1 others  
ORIGIN  
Query Match 96.0%; Score 1851.4; DB 6; Length 1930;  
Best Local Similarity 97.8%; Pred. No. 0;  
Matches 1887; Conservative 0; Mismatches 42; Indels 1; Gaps 1;  
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QY 481 CAGGCGCGCGGTCTGTCTGCTGCTGCTTTGAGGCGATGGATCGTGTAGGGGGAAGACT 540  
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Qy	1501	TCGAGCTGTGACCCCATCTCATTTGCGAGAGATACACAGCATCGAATCGATCGCAATGG	1560
Db	1500	TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACACAGCATCGAATCGATCGCAATGG	1559
Qy	1561	TCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGCAG	1620
Db	1560	TCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGCAG	1619
Qy	1621	GTACGACAAAATGTGTCTGGGACCAACTCCGGCGAGCCTACGAGAACGCCGGGCCCCAA	1680
Db	1620	GTACGACAGAAGTCTGTCTGGAACCAACTCCGGCGAGCCTACGAGAACGCCGGGCCCCAA	1679
Qy	1681	GTCCAGAGCCGGCCAAACGTGCTCGAAATCGAGTGGTCTGAAGCAGCAGTATTTCCAAGGA	1740
Db	1680	GTCCAGAGCCGGCCAAACGTGCTCGAGATCGAGTGGTCTGAAGCAGCAGTATTTCCAAGGA	1739
Qy	1741	GCTCCAGAGCCGCTCTATTGGCTGACGATCTCATACACTGGGTTCGGCGTCTCAGACG	1800
Db	1740	GCGCCAGAGCCGCTCTATTGGCTGAACTGCTCAACACACTGGGTTCGGCGTCTCAGACG	1799
Qy	1801	CCGTTCAAGTGTGTTTCATTTGGTGGAAACGAGACGTCCTTTAGTTTGGAAAGGGTATATG	1860
Db	1800	CCGTTCAAGGGTGTTCATTTGGTGGAAACGAGACGTCCTTTGGTGGAAAGGGTATATG	1859
Qy	1861	GAAGGGCCATACGATCGGCTCAACGAGTCTCTCAGAAGTTGTGCTAGCCTGGTGCCA	1920
Db	1860	GAAGGGCCATACGATCGGCTCAGGAGCGCTCAGAAGTTGTGCTAGCCTGGTGCCA	1919
Qy	1921	GCAGCATAG 1929	
Db	1920	GCAGCATAG 1928	
RESULT 5			
AR145469			
LOCUS			
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KEYWORDS			
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QY	1321	AGCAAAAGGTGGTGGTTTCGGTTACCGACAACATTTGTTATCCACCTTGACATTTTCACCA	1380
Db	1320	AGTAAAGGTGGTGGTTTCGGTTACCGACAACCTTTGTTATCCACCTTGATATTTTCACCA	1379
QY	1381	CTCTTCCCGCGAGAGAAGCAAGCATTTGGCGGAAATCTATCTCGGTACTATAGCAAG	1440
Db	1380	CTCTTCCCGCGAGAGAAGCAAGCATTTGGCTGAANAATCCATCCTGGGTACTATAGCAAG	1439
QY	1441	ATAGTCTTCGTATGGGACAAACCGTGGTGGCGCAACAAAGGTTCTCGGGCGTCTCCCAA	1500
Db	1440	ATAGTCTTCGTATGGGACAAAGCTGTGGTGGCGCAACAAAGGTTCTCGGGCGTCTCCCAA	1499
QY	1501	TCGAGCTGACCCCATCTCATTTGGCCAGAGATACCAGCATCGAAGTCGATCGCAATGG	1560
Db	1500	TCGAGCTGTGACCCCATCTCATTTGGCCAGAGATACCAGCATCGAAGTCGATCGCAATGG	1559
QY	1561	TCCATTACCTGTTTCATGTGCGGAGACCCGGGACGGAAGTGGTCCCAACAGATCCCAAGCAG	1620
Db	1560	TCCATTACCTGTTTCATGTGCGGAGACCCGGGACGGAAGTGGTCCCAACAGATCCCAAGCAG	1619
QY	1621	GTAGCAAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACCGCGGGGCCAA	1680
Db	1620	GTAGCAAGAAGTCTGTCTGGAAACCAACTCCGCGCAGCCTACGAGAACCGCGGGGCCAA	1679
QY	1681	GTCCAGAGCGCGCTATGGGCTGAAGCATCTCATCACACTGGGTTCCGGCGCTCAGAACG	1740
Db	1680	GTCCAGAGCGCGCATGCTGCTGAAGCATCGAGTGGTGGTGAAGCAGCAGTATTTCCAAGGA	1739
QY	1741	GCTCCGAGCGCGTCTATGGGCTGAAGCATCTCATCACACTGGGTTCCGGCGCTCAGAACG	1800
Db	1740	GCGCCGAGCGCGTCTATGGGCTGAAGCATCTCATCACACTGGGTTCCGGCGCTCAGAACG	1799
QY	1801	CCGTTCAAGTGTGTTCAATTCGTTGGAAACGAGACGTCCTTAGTTGGAAAGGTTATATG	1860
Db	1800	CCGTTCAAGGTTGTTCATTTCTGTTGSAACGAGACGTCCTTAGTTGGAAAGGTTATATG	1859
QY	1861	GAAGGGGCATACCATCGGGTCAACAGAGTGTGTCAGAAGTGTGGTACGCTGGTGCCA	1920
Db	1860	GAAGGGGCATACCATCGGGTCAACAGAGTGTGTCAGAAGTGTGGTACGCTGGTGCCA	1919
QY	1921	GCAGCATAG 1929	
Db	1920	GCAGCATAG 1928	
RESULT 6			
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LOCUS			linear
DEFINITION			PAT 08-AUG-2001
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 1847;			
Conservative			
Mismatches			
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Gaps			
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QY	1	ATGGCATTGTCACCGAGCTACATCAATCCCCCAACGTCGCTCCCGCAGGAGGTTATCC	60
Db	1	ATGGCATTGTCACCGAGCTACATCAATCCCCCAACCTCGCCTCCCGCAGGAGGTTATCC	60

QY	61	CACATCGGCGTAGCCCAAAAGGAGCGAGGTATGCTGACAATAGCTGGACAGATTGGACAA	120
Db	61	CACATCGGCGTAGCCCAAAAGGAGGAGGTATGCTGACAATAGCTGGACAGATTGGACAA	120
QY	121	GACGCTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTGGCCCAAGCATTCGCCAAT	180
Db	121	GACGCTTCGGCCGTGACAGACCCCTGCCTACGAGAAACAGGTGGCCCAAGCATTCGCCAAC	180
QY	181	CTGGAGGCTTCGCTGCTGAGTTGGAGCCCTCTTCAACAGCAGCTCACCAAGCTCAATTAC	240
Db	181	CTGGAGGCTTCGCTGCTGAGTTGGAGCCCTCTTCAACAGCAGCTCACCAAGCTCAATTAC	240
QY	241	TACATCTGCTGACTACGCGCCCGAGCAAACTCACCGCAATTTGGAGATGGGCTGAAGCTTACC	300
Db	241	TACATCTGCTGACTACCAACCCGAGCAAACTCACCGCAATTTGGAGATGGGCTGAAGGCTACC	300
QY	301	TTTGGCCCTTGACAGGCTCCCTCTGTCAGCTGGTGGCAGTACCGGCTTGGCTTTCACCT	360
Db	301	TTTGGCCCTTGACAGGCTCCCTCTGTCAGCTGGTGGCAGTACCGGCTTGGCTTTCACCT	360
QY	361	GAATACCTCTTTGAGGTTGATGCCACGCGCTGGTGGCAGCAGCTCGACCCCAAGCAAC	420
Db	361	GAATACCTCTTTGAGGTTGATGCCACGCGCTGGTGGCAGCAGCTCAACCCCAAGCAAT	420
QY	421	GTTGGGAGCTGTAGTGGTGGGCGCTGGCTTGAGCGGTTTGGAGACGCGCACGAAAGTC	480
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QY	481	CAGGCGCGCGGCTGTCTCTGCTGCTGCTTTGAGGCGATGGATCGTGTAGGGGGAAGACT	540
Db	481	CAGGCTGCGGGCTGTCTCTGCTGCTTTGAGGCGATGGATCGTGTGGGGGGAAGACT	540
QY	541	CTGAGCGTACAATCGGTCCTCGGAGGAGCAGCTATCAACAGCTCGCGCTGGCTGGATC	600
Db	541	CTGAGCGTACAATCGGGTCCCGGAGGAGCGGTATCAATGACCTCGCGCTGGCTGGATC	600
QY	601	AATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGCGCGAG	660
Db	601	AATGACAGCAACCAAGCGAAGTATTCAAATTAATTTGAAGATTTCATTTGAGGCGCGAG	660
QY	661	CTCCAGAGCAGCAGCGGAATTCATCCATCAAGCACAAGCGGTACACCACTACAGCT	720
Db	661	CTCCAGAGCAGCAGCGGAATTCATCCATCAAGCACAAGCGGTACACCACTACAGCT	720
QY	721	CCTTATGGTGAATCCCTGGTGAAGCAATTCATCTTGTGATGAGACCTCTGCTGCTGT	780
Db	721	CCTTATGGTGAATCCCTGGTGAAGCAATTCATCTTGTGATGAGACCTCTGCTGCTGT	780
QY	781	AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGGTGGCAAGTCCAGCT	840
Db	781	AGAATACAGTCACTGACTCCCATCTCGAGCTGAGCGAGGAGGTGGCAAGTCCAGCT	840
QY	841	GGAACCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC	900
Db	841	GGAACCTCTCCCGATGGTCTCAGCTGATCGAAGAGTATAGTCTTGAAGACCCCAAGGC	900
QY	901	GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCAGTCTGTGAGAGAGACCT	960
Db	901	GAGCCCTCAAGCGAAGCAGCTCGACAGTGTGAGCTTCGCGCAGTCTGTGAGAGAGATCT	960
QY	961	AAACTTGCCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGA	1020
Db	961	AAAGTTGCCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGA	1020
QY	1021	AGCCACGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTCCACCGGTTCTCAG	1080
Db	1021	AGCCACGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTCCACCGGTTCTCAG	1080
QY	1081	TAATATTGCTCGGACAAAGAAAGCGCGGGGAGTATATCGGATGCAAAACAGGTCGGTG	1140
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QY 1141 CGGTGTCCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCAATCCAGGTATGCAGTCGATT 1200  
Db 1141 TGGTGTCTCTCA-GTGGGAGACTCGTTTCTTAGTGGTCAATCCAGGTATGCAGTCGCTT 1199

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QY 1261 GCAATTGAGCAGTCGGGCTCGGCTGTATAGTACGATCCGCTCGGCGCGCTGTTCGA 1320  
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QY 1321 AGCAAAAAGGTGGTGTTCCTTACCAGAACATTTGATCCCACTTGGACATTTTCAACA 1380  
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QY 1741 GTCCGAGCGCGCTATATGGGCTGAACGATCTCATCACATCGTGGTTCGGCGCTCAGAAG 1800  
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QY 1801 CGGTTCAAGTGTTCATTTCTGGTGAACGAGACGCTTTAGTTTGGAAAGGTTATATG 1860  
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QY 1861 GAAGGGCCATACGATCGGCTCAACGAGGTGCTCGAGAAAGTTGGCTAGCCTGGTGCCA 1920  
Db 1860 GAAGGGCCATACGATCGGCTCAGCGAGCGCTGCAGAAAGTTGGCTAGCCTGGTGCCA 1919

QY 1921 GCAGCATAG 1929  
Db 1920 GCAGCATAG 1928

RESULT 7  
AR14547  
LOCUS AR14547 1803 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 22 from patent US 6211434.  
ACCESSION AR14547  
VERSION AR14547.1 GI:15107324  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1803)  
AUTHORS Duwick,J.P., Gilliam,J.T. and Maddox,J.R.  
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides  
and methods of use  
JOURNAL Patent: US 6211434-A 22 03-APR-2001;  
FEATURES Location/Qualifiers

source 1. 1803  
BASE COUNT 424 a 501 c 502 g 376 t  
ORIGIN  
Query Match 83.1%; Score 1602.6; DB 6; Length 1803;  
Best Local Similarity 91.7%; Pred. No. 0;  
Matches 1769; Conservative 0; Mismatches 34; Indels 126; Gaps 2;  
QY 1 ATGGCACTTGACCCAGCTACATCAATCCCCCAACAGTCGCTCCCCAGCAGGATTC 60  
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RESULT 8  
AR145484 1803 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 22 from patent US 6211435.

ACCESSION AR145484  
VERSION AR145484.1 GI:15107351  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1803)  
AUTHORS Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.  
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides  
and methods of use  
JOURNAL Patent: US 6211435-A 22 03-APR-2001;  
FEATURES Location/Qualifiers  
1..1803  
Source /organism="unknown"  
BASE COUNT 424 a 501 c 502 g 376 t  
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Query Match 83.1%; Score 1602.6; DB 6; Length 1803;  
Best Local Similarity 91.7%; Pred. No. 0;  
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QY 1921 GCAGCATAG 1929  
Db 1795 GCAGCATAG 1803  
RESULT 9  
ARI45462  
LOCUS ARI45462 2490 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 32 from patent US 6211434.  
ACCESSION ARI45462  
VERSION ARI45462.1 GI:15107329  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2490)  
AUTHORS Duvick, J.P., Gilliam, J.T. and Maddox, J.R.  
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides  
and methods of use  
JOURNAL Patent: US 6211434-A 32 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1. 2490  
BASE COUNT 625 a 623 c 653 g 589 t  
ORIGIN  
Query Match 82.7%; Score 1596.2; DB 6; Length 2490;  
Best Local Similarity 91.5%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;  
QY 1 ATGGCACTTGCACGAGGTACATCAATCCCCAAAACCTCGCCTCCCCAGAGGGTATTTC 60  
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Db 2482 GCAGCATAG 2490  
RESULT 10  
AR145489  
LOCUS AR145489 2490 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 32 from patent US 6211435.  
ACCESSION AR145489  
VERSION AR145489.1 GI:15107356  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2490)  
AUTHORS Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.  
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use  
JOURNAL Patent: US 6211435-A 32 03-APR-2001;  
FEATURES  
source Location/Qualifiers  
BASE COUNT 625 a 623 c 653 g 589 t  
ORIGIN  
Query Match 82.7%; Score 1596.2; DB 6; Length 2490;  
Best Local Similarity 91.5%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;  
Qy 1 ATGGCACTTGCACCGAGCTACATCAATCCCAAGCTGCGCTCCCAAGCAGGATATTC 60  
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Db 1128 AAGCAGGTACGACAAAGTCTGTCTGGGACCACTCGGCGCAGCTTACAGAACGCCGG 1187  
QY 1675 GCGCAATGCCAGAGCGCGCAAGCTGCTGGAATCAGTGGTGGAGCAGCAGTATTTC 1734  
Db 1188 GCGCAATGCCAGAGCGCGCAAGCTGCTGGAATCAGTGGTGGAGCAGCAGTATTTC 1247  
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Db 1308 AGAACCGCGTTCAGTGTGTTTCATTGTTGGAAACGAGACGCTTTAGTTTGGAAAGG 1367  
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTG 1914  
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Db 1428 GTGCCAGCAGCATAG 1442

RESULT 13  
LOCUS AR145459 2976 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 26 from patent US 6211434.  
ACCESSION AR145459  
VERSION AR145459.1 GI:15107326  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2976)  
AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.  
TITLE Amino polyol amine oxide polynucleotides and related polypeptides  
and methods of use  
JOURNAL Patent: US 6211434-A 26 03-APR-2001;  
FEATURES  
source Location/Qualifiers  
BASE COUNT 564 a 932 c 926 g 554 t  
ORIGIN  
Query Match 62.8%; Score 1212.2; DB 6; Length 2976;  
Best Local Similarity 90.2%; Pred. No. 1.4e-313;  
Matches 1372; Conservative 0; Mismatches 23; Indels 126; Gaps 2;  
QY 409 ACCCCAGACAAAGTTGCGGACGTGTGTAGTGTGGCGCTGGCTTGGAGCGGTTGGAGACG 468  
Db 1582 AGCAAAAGACAAAGTTGCGGACGTGTGTAGTGTGGCGCTGGCTTGGAGCGGTTGGAGACG 1641  
QY 469 GCACGAAAAGTTCAGGCGCGCGGTCTGTCTGCTGCTTCTTGGAGCGATGGATCGTGA 528  
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Qy	1309	GCGGTGTCGGAAGCAAAAAGTGGTTCGTTACCGACAACATGTATCCACCTTG	1368
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Qy	1489	GGCGTCTCCAAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAATCGAAGTC	1548
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Qy	1729	TATTTCCAAGAGCTCCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGGTCG	1788
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DEFINITION	Sequence 26 from patent US 6211435.		
ACCESSION	AR145486		
VERSION	AR145486.1 GI:15107353		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2976)		
AUTHORS	Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.		
TITLE	Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use		
JOURNAL	Patent: US 6211435-A 26 03-APR-2001;		
FEATURES	Location/Qualifiers		

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ORIGIN	/organism="unknown"		
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Best Local Similarity	90.2%;	Pred. NO. 1.4e-313;	
Matches 1372;	Conservative	0; Mismatches	23; Indels 126; Gaps 2;
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Qy	469	GCACGCAAAAGTCCAGCGCCCGCTGTCTCTCGCTCGTTTCTTGGCGGATGATCGTGA	528
Db	1642	GCACGCAAAAGTCCAGCGCCCGCTGTCTCTCGCTCGTTTCTTGGCGGATGATCGTGA	1701
Qy	529	GGGGAAAGACTCTGAGCGTACAATCGGGTCCCGGACGAGCACTATCAAGACCTCGC	588
Db	1702	GGGGAAAGACTCTGAGCGTACAATCGGGTCCCGGACGAGCACTATCAAGACCTCGC	1761
Qy	589	GCTGCGTGATCAATCACAGCAACCAAGCAAGTATCCAGATTCTTTGAAAGATTTTCA	648
Db	1762	GCTGCGTGATCAATCACAGCAACCAAGCAAGTATCCAGATTCTTTGAAAGATTTTCA	1821
Qy	649	TTGGAGGGCAGCTCCAGAGGACGACCGGAAATTCATTCATCAAGCAACAGCGGTACA	708
Db	1822	TTGGAGGGCAGCTCCAGAGGACGACTGGAATTCATTCATCAAGCAACAGCGGTACA	1881
Qy	709	ACACTACAGCTCCTTATGGTGACTCCCGGTAAGCAACAATCCCACTTTGTGATGAGAC	768
Db	1882	ACACTACAGCTCCTTATGGTGACTC-----	1907
Qy	769	TCTGTCGAGTGTAGATACAGTCACTCCACTTCGTCAGCTGAGCGAGAGGTTGC	828
Db	1908	-----CTTGCTGAGCGAGAGGTTGC	1928
Qy	829	AAGTGCACTTGGGAACTCCTCCCGTATGTCTCAGCTGTATCGAAGATATAGCCTTGA	888
Db	1929	AAGTGCACTTGGGAACTCCTCCCGTATGTCTCAGCTGTATCGAAGATATAGCCTTGA	1988
Qy	889	AGACCCCAAGGGAGCGCTCAGCGAAGCGCTGCAGTGTGAGCTTCGCCCACTACTG	948
Db	1989	AGACCTTCAAGGGAGCGCTCAGCGAAGCGCTGCAGTGTGAGCTTCGCCCACTACTG	2048
Qy	949	TGAGAAGGACCTAAACTTCGCTTCTCAGCGTGGCAACACAGATCACACGCGTCT	1008
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Qy	1009	GCTCGGTGGGAAGCCCAAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGC	1068
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Db	2229	AA-----CAGGT	2235
Qy	1189	ATGCAGTCGATTTGCCATGCCATGTCAAGGAACCTTGTTCAGGCTCAGTGCACCTCAAC	1248
Db	2236	ATGCAGTCGATTTGCCATGCCATGTCAAGGAACCTTGTTCAGGCTCAGTGCACCTCAAC	2295
Qy	1249	ACCCCGTCCGTGGAATTGAGCAGTCGCGCTCGCGCTGTATAGTACGATCGGCTCGGC	1308
Db	2296	ACCCCGTCCGTGGAATTGAGCAGTCGCGCTCGCGCTGTATAGTACGATCGGCTCGGC	2355
Qy	1309	GCGGTGTCGGAAGCAAAAAGTGGTTCGTTACCGACAACATGTATCCACCTTG	1368
Db	2356	GCGGTGTCGGAAGCAAAAAGTGGTTCGTTACCGACAACCTTGTATCCACCTTG	2415

QY	1369	ACATTTTACCACCTCTTCCGCGCAGAGCAAGCATTTGGCGAAAAATCTATCCTCGG	1428
Db	2416	ACATTTTACCACCTCTTCCGCGCAGAGCAAGCATTTGGCGAAAAATCTATCCTCGGC	2475
QY	1429	TACTATAGCAAGATAGTCTTTCGTATGGGACAAACCGTGTGGCGCAACAAGCTTCTCG	1488
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QY	1489	GGCGTCTCCAANTCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGCATCGAAGTC	1548
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QY	1729	TATTTCCAAGAGCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTGG	1788
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DEFINITION Sequence 24 from patent US 6211434.			
ACCESSION AR145458			
VERSION AR145458.1 GI:15107325			
KEYWORDS			
SOURCE Unknown.			
ORGANISM Unknown.			
REFERENCE 1 (bases 1 to 3003)			
AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.			
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides			
JOURNAL Patent: US 6211434-A 24 03-APR-2001;			
FEATURES Location/Qualifiers			
source 1..3003			
BASE COUNT 690 a 840 c 819 g 654 t			
ORIGIN /organism="unknown"			
Query Match 62.8%; Score 1212.2; DB 6; Length 3003;			
Best Local Similarity 90.2%; Pred. No. 1.4e-313;			
Matches 1372; Conservative 0; Mismatches 23; Indels 126; Gaps 2;			
QY	409	ACCCACAGAACGTTCCGACGTGTAGTGTGGCGCTGGCTTGAGCGGTTTGAGACG	468
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QY	469	GCACGCAAGTCCAGCGCCCGGTCTGCTCCCTGCTTCTTGAGCGCATGATCGTGTA	528
Db	1669	GCACGCAAGTCCAGCGCCCGGTCTGCTCCCTGCTTCTTGAGCGCATGATCGTGTA	1728

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Db	1729	GGGGGAAAGACTCTGAGCGTACAATCGGTCGCCGAGGACGACTATCAACAGCCTCGGC	1788
QY	589	GCTGCGTGATCAATGACAGCAACCAAGCGAAGTATCCACATTTGTTGAAGATTTTCAT	648
Db	1789	GCTGCGTGATCAATGACAGCAACCAAGCGAAGTATCCACATTTGTTGAAGATTTTCAT	1848
QY	649	TTGGAGGCGAGCTCCAGAGGACGACCGGAAATTCATATCCATCAAGCACAAAGCGGTACA	708
Db	1849	TTGGAGGCGAGCTCCAGAGGACGACGCGAAATTCATATCCATCAAGCACAAAGCGGTACA	1908
QY	709	ACCACTACAGCTCCTTATGTGTGACTCCCGGTAAAGACAATCCCACTTTGTGTGATGAGCC	768
Db	1909	ACCACTACAGCTCCTTATGTGTGACTCCCGGTAAAGACAATCCCACTTTGTGTGATGAGCC	1934
QY	769	TCTGTGAGTGTAGAATACAGTCACTGACTCCACTTCTGTCAGCTGAGCGAGGAGTTGC	828
Db	1935	-----CTTGTGAGCGAGGAGTTGC	1955
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QY	889	AGACCCCAAGCGGAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGGGCACACTG	948
Db	2016	AGACCTCAAGCGGAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGGGCACACTG	2075
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QY	1249	ACCCCGTTCGCTGGAATTGAGCAGTCGGCTCGGCTGTATAGTACGATCGGCTCGGGC	1308
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Db	2563	GGGCTCTCCAATGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGCATCGAAGTC	2622
QY	1549	GATCGCAATGGTCCATTAACCTGTTTCATGTCGGAGACCCGGAGCGAAGTGGTCCCAA	1608
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QY	1609	CAGTCCAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGGCGAGCCTACGAGAAC	1668
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QY	1669	GCGGGGGCCCAAGTCCGAGAGCCGGCCCAACGTGCTCGAAATCGAGTGTCTGAAAGCAGCAG	1728
Db	2743	GCGGGGGCCCAAGTCCGAGAGCCGGCCCAACGTGCTCGAAATCGAGTGTCTGAAAGCAGCAG	2802
QY	1729	TATTTCCAAGGAGCTCCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCTG	1788
Db	2803	TATTTCCAAGGAGCTCCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCTG	2862
QY	1789	GCGCTCAGAACCCGTTCAAGTGTCTTCATTTCGTTGGAACGGAGACGTCCTTTAGTTTGG	1848
Db	2863	GCGCTCAGAACCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCCTTTAGTTTGG	2922
QY	1849	AAAGGTATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAAGAGTTGTGGCT	1908
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Job time : 5111 secs





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OM nucleic - nucleic search, using sw model

Run on: November 12, 2002, 02:14:19 ; Search time 416 Seconds  
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10442.560 Million cell updates/sec

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Perfect score: 1929  
Sequence: 1 atggcaactgcaccagagcta.....gccttggtgccagcagcatag 1929

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	1925.8	99.8	1929	21	AAZ58383 Exophiala spinifer
3	1851.4	96.0	1930	21	AAZ58384 Exophiala spinifer
4	1792.2	92.9	1928	21	AAZ58386 Rhinocladiaella atr
5	1789	92.7	1928	21	AAZ58387 Rhinocladiaella atr
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9	1596.2	82.7	2490	21	AAZ58407 DNA encoding GST-t

10	1596.2	82.7	2490	21	AAZ60646 DNA encoding a fus
11	1319	68.4	1442	21	AAZ58393 Amino polyol amine
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13	1212.2	62.8	2976	21	AAZ58404 DNA encoding funon
14	1212.2	62.8	2976	21	AAZ60643 DNA encoding a fus
15	1212.2	62.8	3003	21	AAZ58403 DNA encoding funon
16	1212.2	62.8	3003	21	AAZ60642 DNA encoding a fus
17	1212.2	62.8	3591	21	AAZ58406 DNA encoding funon
18	1212.2	62.8	3591	21	AAZ60645 DNA encoding a fus
19	1212.2	62.8	3618	21	AAZ58405 DNA encoding funon
20	1212.2	62.8	3618	21	AAZ60644 DNA encoding a fus
21	1212	62.8	1392	21	AAZ58394 Amino polyol amine
22	1212	62.8	1392	21	AAZ60633 DNA encoding an am
23	1212	62.8	1464	21	AAZ58401 DNA encoding amino
24	1212	62.8	1464	21	AAZ60640 DNA encoding an am
25	1212	62.8	1673	21	AAZ58395 Amino polyol amine
26	1212	62.8	1673	21	AAZ60638 DNA encoding an am
27	1212	62.8	2079	21	AAZ58400 DNA encoding GST-t
28	1212	62.8	2079	21	AAZ60639 DNA encoding an am
29	1211	62.8	1389	21	AAZ58392 Amino polyol amine
30	1211	62.8	1389	21	AAZ60630 DNA encoding an am
31	361.4	18.7	372	21	AAZ58388 Exophiala spinifer
32	361.4	18.7	372	21	AAZ60654 Nucleotide sequenc
33	174	9.0	182	21	AAZ58389 Nucleotide sequenc
34	174	9.0	182	21	AAZ60663 Propionibacterium
35	49.2	2.6	66788	23	AAZ59515 Human monoamine ox
36	40.8	2.1	1619	22	AAF62793 Gene #2392 used to
37	40.8	2.1	2491	22	AAF62783 Lung cancer relate
38	40.8	2.1	2491	24	ABN95894 Kidney cancer rela
39	40.8	2.1	2491	24	ABL66273 Micrococcal putres
40	40.8	2.1	2491	24	ABL68529 Mycobacterium tube
41	40.8	2.1	2386	15	AAQ63477 Drosophila melanog
42	40.4	2.1	1347	22	AAC97010 Drosophila melanog
43	40.2	2.1	1347	22	AAC97010 Drosophila melanog
44	39.4	2.0	3559	23	ABL23641 Drosophila melanog
45	39.4	2.0	3645	23	ABL18747 Drosophila melanog

ALIGNMENTS

RESULT 1

AAZ58382

ID AAZ58382 standard; DNA; 1929 BP.

XX

AC AAZ58382;

XX

DT 23-MAY-2000 (first entry)

XX

DE Exophiala spinifera amino polyol amine oxidase ESP002\_C2 DNA.

XX Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;

KW detoxification; animal feed; silage; selectable marker; ds.

XX Exophiala spinifera.

OS Exophiala spinifera.

XX Key Location/Qualifiers

FT CDS 1..1929

FT /tag= a

FT /note= "contains introns"

FT intron 739..811

FT /tag= b

FT intron 1134..1186

FT /tag= c

XX WO200004159-A1.

XX

PN 27-JAN-2000.

XX

XX 08-JUL-1999; 99WO-US15454.

XX

XX 15-JUL-1998; 98US-0092936.

XX

XX 21-MAY-1999; 99US-0135391.

PR

XX (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
PI Duwick JP, Gilliam JT, Maddox JR;  
XX WPI; 2000-182425/16.  
DR P-PSDB; AAY58900.  
XX New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading fumonisin or structurally related mycotoxin in processed  
PT grain or in silage -  
XX Claim 1; Page 137-138; 154pp; English.  
XX The present sequence is that of an isolated nucleic acid,  
CC designated Esp002.C2, of *Exophiala spinifera* isolate Esp002,  
CC which encodes an amino polyol amine oxidase (APO, see AAY58900)  
CC capable of degrading fumonisin, its hydrolysis product API, and  
CC related mycotoxins. The DNA was obtained by PCR amplification of  
CC Esp002 mycelial DNA using primers based on APO of *E. spinifera*  
CC AAY58900 (see AAY58900-05) of *E. spinifera* and  
CC Rhinocladiella atrovirens. The polynucleotides are used to transform  
CC plant cells normally susceptible to Fusarium or other toxin-producing  
CC fungus infection. Transgenic plants can be regenerated from the  
CC transformed plant cells. Also provided are methods for expressing  
CC both APO and a fumonisin-esterase in a transgenic plant, and for  
CC producing APO enzyme in prokaryotic and non-plant eukaryotic  
CC systems. Transgenic plants capable of degrading fumonisin or of  
CC producing the degrading enzymes are provided. Methods for  
CC detoxification of grain, grain processing, silage, food crops and  
CC in animal feed and rumen microorganisms are also disclosed. APO  
CC polynucleotide is also useful as a selectable marker.  
XX Sequence 1929 BP; 451 A; 537 G; 532 G; 409 T; 0 other;  
Query Match 100.0%; Score 1929; DB 21; Length 1929;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAGCTTGACCGAGCTACATCAATCCCAACCTCGCTCCCGCAGGAGTATTC 60  
DB 1 ATGGCAGCTTGACCGAGCTACATCAATCCCAACCTCGCTCCCGCAGGAGTATTC 60  
QY 61 CACATCGGCGTAGGCCAAACGACGAGGTATGTGACATAGCTGGACAGATTGGACAA 120  
DB 61 CACATCGGCGTAGGCCAAACGACGAGGTATGTGACATAGCTGGACAGATTGGACAA 120  
QY 121 GACGCTTTGGGGGTGACAGACCCAGCTTACGAGAAACAGGTGCCCCAAGCATTCGCGCAAT 180  
DB 121 GACGCTTTGGGGGTGACAGACCCAGCTTACGAGAAACAGGTGCCCCAAGCATTCGCGCAAT 180  
QY 181 CTGCGAGCTTGCGTTGCTGCAAGTGGAGCCCTCTTCAACGACGCTCACCAAGCTCAATTAC 240  
DB 181 CTGCGAGCTTGCGTTGCTGCAAGTGGAGCCCTCTTCAACGACGCTCACCAAGCTCAATTAC 240  
QY 241 TACATCGTCGACTAGCCCGCCGAGCAAACTACCCCAATTGGAGATGGGCTGAAGTCTACC 300  
DB 241 TACATCGTCGACTAGCCCGCCGAGCAAACTACCCCAATTGGAGATGGGCTGAAGTCTACC 300  
QY 301 TTTGGCCCTTGACAGGCTCCCTCTTGGACGCTGGTGCCAGTACCGGCTTGGCTTCACCT 360  
DB 301 TTTGGCCCTTGACAGGCTCCCTCTTGGACGCTGGTGCCAGTACCGGCTTGGCTTCACCT 360  
QY 361 GAATACCTCTTTGAGTTGATGCCAGCGGCTGTGTGCCAGGACACTCGACCCGAGCAAC 420  
DB 361 GAATACCTCTTTGAGTTGATGCCAGCGGCTGTGTGCCAGGACACTCGACCCGAGCAAC 420  
QY 421 GTTGGGACGTTGGTAGTGGTGGGCGCTGGCTTGGAGCGGTTGGAGAGCGGCAAGATC 480  
DB 421 GTTGGGACGTTGGTAGTGGTGGGCGCTGGCTTGGAGCGGTTGGAGAGCGGCAAGATC 480

QY 481 CAGGCCGCGGCTGTCTGCTCCTCGTTCCTTCTTGGAGCGATGATCGTGTAGGGGGAAGACT 540  
DB 481 CAGGCCGCGGCTGTCTGCTCCTCGTTCCTTCTTGGAGCGATGATCGTGTAGGGGGAAGACT 540  
QY 541 CTGAGCGTACAAATCGGGTCCCGGAGGAGCACTATCAACGACCTCGGCGCTCGGTGGATC 600  
DB 541 CTGAGCGTACAAATCGGGTCCCGGAGGAGCACTATCAACGACCTCGGCGCTCGGTGGATC 600  
QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATTTGTTGAAAGATTTTCATTTGGAGGCGGAG 660  
DB 601 AATGACAGCAACCAAGCGAAGTATCCAGATTTGTTGAAAGATTTTCATTTGGAGGCGGAG 660  
QY 661 CTCAGAGGAGCGCGGAAATTCATCCATCAAGCACAGACGGTACAAACCACCTACAGCT 720  
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QY 721 CCTTATGTGACTCCCGGTAAGCACAAATCCCACTTTGTGATGAGACCTCTGTGCGAGTGT 780  
DB 721 CCTTATGTGACTCCCGGTAAGCACAAATCCCACTTTGTGATGAGACCTCTGTGCGAGTGT 780  
QY 781 AGAATACAGTCACTGACTCCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCATTCG 840  
DB 781 AGAATACAGTCACTGACTCCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCATTCG 840  
QY 841 GGAATCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGGC 900  
DB 841 GGAATCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGGC 900  
QY 901 GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTGGCGCACTACTGTGAGAGGACCT 960  
DB 901 GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTGGCGCACTACTGTGAGAGGACCT 960  
QY 961 AAATCTGCTCTGCTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGGA 1020  
DB 961 AAATCTGCTCTGCTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGGA 1020  
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DB 1021 AGCCACAGATCAGCATGCTTTTCTCACCGCTACATCAAGAGTGCACACCGGTCTCAG 1080  
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QY 1261 GGAATTGAGCAGTCCGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCGTGTCCGA 1320  
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DB 1321 AGCAAAAGGTGGTGGTTTCTTACCCAGCAACATTGTATCCGACCTTGACATTTTCCACA 1380  
QY 1381 CCTCTTCCCGCGAGAAAGCAAGCATTTGGCGGAAAAATCTATCTCGGCTACTATAGCAAG 1440  
DB 1381 CCTCTTCCCGCGAGAAAGCAAGCATTTGGCGGAAAAATCTATCTCGGCTACTATAGCAAG 1440  
QY 1441 ATAGTCTTCGTATGGGACACCCGTTGGTGGGCGAACAGGCTTCTCGGCGCTCTCCAA 1500  
DB 1441 ATAGTCTTCGTATGGGACACCCGTTGGTGGGCGAACAGGCTTCTCGGCGCTCTCCAA 1500  
QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGCATCGAAGTTCGATCGGCAATGG 1560  
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QY 1561 TCCATTACCTCTTTTCATGGTGGGAGACCCGGGAGCGGAAGTGGTCCCAACAGTCCCAAGCAG 1620

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Db 1561 TCCATTACCTGTTTCATGTCGGAGACCCGGGACGGGAAGTGGTCCCNACAGTCCAAGCAG 1620  
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Db 1921 GCAGCATAG 1929  
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RESULT 2  
AAZ58383  
ID AAZ58383 standard; DNA; 1929 BP.  
XX  
AC AAZ58383;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Exophiala spinifera amino polyol amine oxidase ESP002\_C3 DNA.  
XX  
KW Amino polyol amine oxidase; funonisin; mycotoxin; transgenic plant;  
KW detoxification; animal feed; silage; selectable marker; ds.  
XX  
OS Exophiala spinifera.  
FH Key Location/Qualifiers  
FT CDS 1..1929  
FT /tag= a  
FT /note= "contains introns"  
FT intron 739..811  
FT intron /tag= b  
FT intron 1134..1186  
FT /tag= c  
XX  
PN WO200004159-A1.  
XX  
PD 27-JAN-2000.  
XX  
PF 08-JUL-1999; 99WO-US15454.  
XX  
PR 15-JUL-1998; 98US-0092936.  
PR 21-MAY-1999; 99US-0135391.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
XX  
PI Duvick JP, Gilliam JT, Maddox JR;  
XX  
DR WPI; 2000-182425/16.  
DR P-PSDB; AAZ58901.  
XX  
PT New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading funonisin or structurally related mycotoxin in processed  
PT grain or in silage  
XX

PS Claim 1; Page 139-140; 154pp; English.  
XX  
CC The present sequence is that of an isolated nucleic acid,  
CC designated ESP002\_C3, of Exophiala spinifera isolate ESP002,  
CC which encodes an amino polyol amine oxidase (APAO, see AAY58901)  
CC capable of degrading funonisin, its hydrolysis product API, and  
CC related mycotoxins. The DNA was obtained by PCR amplification of  
CC ESP002 mycelial DNA using primers based on APAO of E. spinifera  
CC ATCC 74269. The invention provides APAO polynucleotides (see  
CC AAZ58383-87) and polypeptides (see AAY58900-05) of E. spinifera and  
CC Rhinocladiella atrovirens. The polynucleotides are used to transform  
CC plant cells normally susceptible to Fusarium or other toxin-producing  
CC fungus infection. Transgenic plants can be regenerated from the  
CC transformed plant cells. Also provided are methods for expressing  
CC both APAO and a funonisin-esterase in a transgenic plant, and for  
CC producing APAO enzyme in prokaryotic and non-plant eukaryotic  
CC systems. Transgenic plants capable of degrading funonisin or of  
CC producing the degrading enzymes are provided. Methods for  
CC detoxification of grain, grain processing, silage, food crops and  
CC in animal feed and rumen microorganisms are also disclosed. APAO  
CC polynucleotide is also useful as a selectable marker.  
XX  
SQ Sequence 1929 BP; 451 A; 539 C; 532 G; 407 T; 0 other;  
Query Match 99.8%; Score 1925.8; DB 21; Length 1929;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1927; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGGCACTTGACCGAGCTACATCAATCCCCAAAGCTCGCTCCGCCACGAGGTATTC 60  
Db 1 ATGGCACTTGACCGAGCTACATCAATCCCCAAAGCTCGCTCCGCCACGAGGTATTC 60  
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Db 781 AGAATACAGTACTGACTCCACTTCGCTCCAGCTGAGCGAGAGGTTGCCAAGTGCACCTTGC 840  
QY 841 GGAACCTCCCTCCCGTATGCTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900  
Db 841 GGAACCTCCCTCCCGTATGCTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900  
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Db 901 GAGCCCTCAGCGCAAGCGGCTGACAGTGTGAGCTTTCGGGCACCTACTGTGAGAAGACCT 960  
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Db 1021 AGCCACGAGATCAGCATGCTTTTCTCACCAGCTACATCAAGAGTGCACCGGCTCTCAG 1080  
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QY 1561 TCCATTACCTGTTTTCATGCTCGGAGACCGGAGCGAAGTGTGCTCCCAAGTCCCAAGCAG 1620  
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QY 1741 GCTCCGAGCGCGCTATGGGTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG 1800  
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Db 1741 GCTCCGAGCGCGTCTATGGGTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG 1800  
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Db 1801 CCGTTCAAGTGTGTTCAATTTGTTGGAACGGAGAGCGTCTTTAGTTTGGAAAGGTATATG 1860  
QY 1861 GAAAGGGCCATACGATCGGTTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920  
Db 1861 GAAAGGGCCATACGATCGGTTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920  
QY 1921 GCAGCATAG 1929  
Db 1921 GCAGCATAG 1929  
RESULT 3  
AAZ58384  
ID AAZ58384 standard; DNA; 1930 BP.  
XX  
AC AAZ58384;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Exophiala spinifera amino polyol amine oxidase ESP003\_C12 DNA.  
XX  
KW Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;  
KW detoxification; animal feed; silage; selectable marker; ds.  
XX  
OS Exophiala spinifera.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1930  
FT /tag= a  
FT /note= "contains introns"  
FT intron 739..811  
FT /tag= b  
FT intron 1134..1187  
FT /tag= c  
XX WO200004159-A1.  
PN  
XX  
PD 27-JAN-2000.  
XX  
PF 08-JUL-1999; 99WO-US15454.  
XX  
PR 15-JUL-1998; 98US-0092936.  
PR 21-MAY-1999; 99US-0135391.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
XX  
PI DuVick JP, Gilliam JT, Maddox JR;  
XX  
DR WPI; 2000-182425/16.  
DR P-PSDB; AAY58902.  
XX  
PT New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading fumonisin or structurally related mycotoxin in processed  
PT grain or in silage  
XX  
PS Claim 1; Page 141-142; 154pp; English.  
XX  
CC The present sequence is that of an isolated nucleic acid,  
CC designated ESP003\_C12, of Exophiala spinifera isolate ESP002,  
CC which encodes an amino polyol amine oxidase (APAO, see AAY58902)  
CC capable of degrading fumonisin, its hydrolysis product API, and  
CC related mycotoxins. The DNA was obtained by PCR amplification of  
CC ESP003 mycelial DNA using primers based on APAO of E. spinifera  
CC AFCC 74269. The invention provides APAO polynucleotides (see  
CC AAZ58383-87) and polypeptides (see AAY58900-05) of E. spinifera and  
CC Rhinocladiella atrovirens. The polynucleotides are used to transform  
CC plant cells normally susceptible to Fusarium or other toxin-producing  
CC fungus infection. Transgenic plants can be regenerated from the

transformed plant cells. Also provided are methods for expressing both APAO and a fumonisin-esterase in a transgenic plant, and for producing APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO polynucleotide is also useful as a selectable marker.

XX Sequence 1930 BP; 449 A; 531 C; 537 G; 412 T; 1 other;

Query Match 96.0%; Score 1851.4; DB 21; Length 1930;  
Best Local Similarity 97.8%; Pred. No. 0;  
Matches 1887; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 1 ATGGCAGTTCACCGAGCTACATCAATCCCAACCTCGCTCCCGCAGGAGTATTC 60  
DB 1 ATGGCAGTTCACCGAGCTACATCAATCCCAACCTCGCTCCCGCAGGAGTATTC 60  
QY 61 CACATCGCGGTAGGCCAAAGCAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120  
DB 61 CACGTGCGGTAGGCCAGAGCGAGGAGGTATGTGACATAGCTGGACAGATTGGACAA 120  
QY 121 GACGTTTGGCGGTGACAGACCGACCTTACGAGAAACAGGTTGCCAAGCATTCGCCAAT 180  
DB 121 GACGTTTGGCGGTGACAGACCGCTCCCTTACGAGAAACAGGTTGCCAAGCATTCGCCAAT 180  
QY 181 CTGGCAGCTTCGCTGTGTCAGTTGGAGCCCTTCAACGACGTCACCAAGCTCAATTAC 240  
DB 181 CTGGCAGCTTCGCTGTGTCAGTTGGAGCCACTTCAACGACGTCACCAAGCTCAATTAC 240  
QY 241 TACATCGTCGACTAGCCCGCAGCAAACTACCGCAATTTGAGATGGGCTGAAGTCTACC 300  
DB 241 TACATCGTCGACTAGCCCGCAGCAAACTACCGCAATTTGAGATGGGCTGAAGGCTACC 300  
QY 301 TTGTCCTTTGACAGCTCCCTCTTGCACGCTGTGTGCCAGTACCGGCTTGGGCTTCACCT 360  
DB 301 TTGTCCTTTGACAGCTCCCTCTTGCACGCTGTGTGCCAGTGTGCGGCTTGTCTTCACCT 360  
QY 361 GAATACCTCTTTGAGTTGATGCCAGCGCTGTGTGCCAGACACTCGACCCAGACAAC 420  
DB 361 GAATACCTCTTTGAGTTGATGCCAGCGCTGTGTGCCAGACACTCGACCCAGACAAC 420  
QY 421 GTTGGGACGTGGTAGTGGTGGGCGCTGGCTTGAGCGGTTTGGAGCGGCACGCAAAAGTC 480  
DB 421 GTTGGGACGTGGTAGTGGTGGGCGCTGGCTTGAGCGGTTTGGAGCGGCACGCAAAAGTC 480  
QY 481 CAGGCGCGGCTGTCTGCTGCTGTCTTGTAGCGGATGGATCTGTAGGGGGAAAGACT 540  
DB 481 CAGGCGCGGCTGTCTGCTGCTGTCTTGTAGCGGATGGATCTGTAGGGGGAAAGACT 540  
QY 541 CTGACGCTACAAATCGGFTCCCGGAGGACGACTATCAACGACCTCGCGCTGCGTGGATC 600  
DB 541 CTGACGCTACAAATCGGFTCCCGGAGGACGACTATCAACGACCTCGCGCTGCGTGGATC 600  
QY 601 AATGACGAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCATTTGGAGGGCGAG 660  
DB 601 AATGACGAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCATNTGGAGGGCGAG 660  
QY 661 CTCGAGAGCAGCGGAAATTCATTCATCAAGCACAAGACGGTACACCACTACAGCT 720  
DB 661 CTCGAGAGCAGCTGGAATTCATTCATCAAGCACAAGACGGTACAACTACAGCT 720  
QY 721 CCTTATGTTGACTCCCGGTGAGCAATCCACTTTTGTGATGAGCTCTGTGAGTGT 780  
DB 721 CCTTATGTTGACTCTTGGTAGCAACAATCCCACTTTTGTGATGAGCTCTGTGAGTGT 780  
QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCACTTGC 840  
DB 781 AGAATACAGTCACTGATTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCACTTGC 840  
QY 841 GGAATCTCTCCCGTATGGTCTGAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900  
|||||

DB 841 GGAATCTCTCCCGTATGGTCTCAGCTGATCGAAGAGCATAGCCTTCAAGACCTCAAGGC 900  
QY 901 GAGCCCTCAGGCGAAGCGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGCACT 960  
DB 901 GAGCCCTCAGGCGAAGCGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGCACT 960  
QY 961 AAACCTTGCCTGCTGTTTCTCAGCGTGCAAAACAGATCACACGCGCTCTGCTCGGTGTGA 1020  
DB 961 AAACCTTGCCTGCTGTTTCTCAGCGTAGCAAAACAGATCACACGCGCTCTGCTCGGTGTGA 1020  
QY 1021 AGCCACAGAGATCAGCATGCTTTTCTCACGACTACATCAAGAGTGCACCGGTCTCAG 1080  
DB 1021 AGCCACAGAGATCAGCATGCTTTTCTCACGACTACATCAAGAGTGCACCGGTCTCAG 1080  
QY 1081 TAATATTGCTCGGACAAGAAAGACGGCGGAGTATATGCGATGCAAAACAGGTGCGGTG 1140  
DB 1081 TAATATTGCTCGGACAAGAAAGACGGCGGAGTATATGCGATGCAAAACAGGTGCGGTG 1140  
QY 1141 CGGTGCTCTCAGSTAGGGGACTCGTTTCT-TAGTGGTCAATTCAGAGTATCGAGTCGAT 1199  
DB 1141 TGGTGTGCTCAGSTAGGGGACTCGTTTCTCAAGTGGTCAATTCAGGTATCGAGTCGAT 1200  
QY 1200 TTGCCATGCCATGTCAAAGAACTTGTCCAGGCTCAGTGCACCTCAACACCCCGTGC 1259  
DB 1201 TTGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTGC 1260  
QY 1260 TGGAAATTGAGCAGTCGCGCTGTATAGTACGATCGGCTCGGGCGCGGTGTTCCG 1319  
DB 1261 TGAATTTGAGCAGTCGCGCATCCGGCTGTACGATCGATCGGCTCGGGCGCGGTGTTCCG 1320  
QY 1320 AAGCAAAAAGGTGGTGGTTTCCGTACCGACAACATTTGTATCCACCTTGACATTTTCACC 1379  
DB 1321 AAGCAAAAAGGTGGTGGTTTCCGTACCGACAACCTTTGTATCCACCTTGACATTTTCACC 1380  
QY 1380 ACCTTTCGCGCGAGAGCAAGCATTTGGCGAAATATCTCTCGGCTACTATAGCAA 1439  
DB 1381 ACCTTTCGCGCGAGAGCAAGCATTTGGCGAAATATCTCTCGGCTACTATAGCAA 1440  
QY 1440 GATAGTCTTGTATGAGCAACCCGTTGGCGCAACAGGCTTCTCGGGCGTCTCCA 1499  
DB 1441 GATAGTCTTGTATGAGCAACCCGTTGGCGCAACAGGCTTCTCGGGCGTCTCCA 1500  
QY 1500 ATCAGCTGTGACCCCATCTCATTTGCCAGAGATACAGCATCGAAGTCGATCGCAATG 1559  
DB 1501 ATCAGCTGTGACCCCATCTCATTTGCCAGAGATACAGCATCGAGTCGATCGACAATG 1560  
QY 1560 GTCCATTACCTGTTTATGTCGGAGACCCGGACGGAAGTGGTCCCAACAGTCCAAAGCA 1619  
DB 1561 GTCCATTACCTGTTTATGTCGGAGACCCGGACGGAAGTGGTCCCAACAGTCCAAAGCA 1620  
QY 1620 GGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTACGAGAAGCGGGGCCCA 1679  
DB 1621 GGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTACGAGAAGCGGGGCCCA 1680  
QY 1680 AGTCCGAGAGCGGCAACGCTCTCGAAATCGAGTGGTGGTGGAGCAGCATTTTCCAAG 1739  
DB 1681 AGTCCGAGAGCGGCAACGCTCTCGAAATCGAGTGGTGGTGGAGCAGCATTTTCCAAG 1740  
QY 1740 AGTCCGAGAGCGGCTATGCGGCTGAACGATCTCATCACACTGGGTTCCGCGCTCAGAC 1799  
DB 1741 AGTCCGAGAGCGGCTATGCGGCTGAACGATCTCATCACACTGGGTTCCGCGCTCAGAAC 1800  
QY 1800 GCCGTTCAAGTGTGTTTCAATTCGTTGGAACGGAGCTCTTTAGTTTGAAGGGTATAT 1859  
DB 1801 GCCGTTCAAGTGTGTTTCAATTCGTTGGAACGGAGCTCTTTAGTTTGAAGGGTATAT 1860  
QY 1860 GGAAGGGCCATACGATCGGGTCAACAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGC 1919  
DB 1861 GGAAGGGCCATACGATCGGGTCAACAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGC 1920  
QY 1920 AGCAGCATAG 1929  
DB 1921 AGCAGCATAG 1930  
|||||

RESULT 4	Matches 1850; Conservative 0; Mismatches 78; Indels 1; Gaps 1;
AAZ58386	
ID AAZ58386 standard; DNA; 1928 BP.	
XX	
AC AAZ58386;	
XX	
DT 23-MAY-2000 (first entry)	
XX	
DE Rhinocladiaella atrovirens amino polyol amine oxidase RAT011-C2 DNA.	
XX	
KW Amino polyol amine oxidase; fumonisln; mycotoxin; transgenic plant;	
KW detoxification; animal feed; silage; selectable marker; ds.	
XX	
OS Rhinocladiaella atrovirens.	
XX	
FH Key	Location/Qualifiers
FT CDS	1..1928
FT	/*tag= a
FT	/note= "contains introns"
FT	739..811
FT	intron
FT	/*tag= b
FT	1134..1186
FT	intron
FT	/*tag= c
XX	
PN WO200004159-A1.	
XX	
PD 27-JAN-2000.	
XX	
PF 08-JUL-1999; 99WO-US15454.	
XX	
PR 15-JUL-1999; 98US-0092936.	
PR	21-MAY-1999; 98US-0135391.
XX	
PA (PION-) PIONEER HI-BRED INT INC.	
PA (CURA-) CURAGEN CORP.	
PI	
PI Duvick JP, Gilliam JT, Maddox JR;	
XX	
DR WPI; 2000-182425/16.	
DR	P-PSDB; AAY58904.
XX	
XX New isolated polynucleotides, polypeptides useful for detecting and	
PT degrading fumonisln or structurally related mycotoxin in processed	
PT grain or in silage	
XX	
PS Claim 1; Page 145-146; 154pp; English.	
XX	
CC The present sequence is that of an isolated nucleic acid,	
CC designated RAT011-C2, of Rhinocladiaella atrovirens isolate RAT011,	
CC which encodes an amino polyol amine oxidase (APAO), see AAY58904)	
CC capable of degrading fumonisln, its hydrolysis product APl, and	
CC related mycotoxins. The DNA was obtained by PCR amplification of	
CC RAT011 mycelial DNA using primers based on APAO of E. spinifera	
CC ATCC 74269. The invention provides APAO polynucleotides (see	
CC AAY58383-87) and polypeptides (see AAY58900-05) of R. atrovirens and	
CC Exophiala spinifera. The polynucleotides are used to transform	
CC plant cells normally susceptible to Fusarium or other toxin-producing	
CC fungus infection. Transgenic plants can be regenerated from the	
CC transformed plant cells. Also provided are methods for expressing	
CC both APAO and a fumonisln-esterase in a transgenic plant, and for	
CC producing APAO enzyme in prokaryotic and non-plant eukaryotic	
CC systems. Transgenic plants capable of degrading fumonisln or of	
CC producing the degrading enzymes are provided. Methods for	
CC detoxification of grain, grain processing, silage, food crops and	
CC in animal feed and rumen microorganisms are also disclosed. APAO	
CC polynucleotide is also useful as a selectable marker.	
XX	
SQ Sequence 1928 BP; 450 A; 527 C; 534 G; 417 T; 0 other;	
Query Match 92.9%; Score 1792.2; DB 21; Length 1928;	
Best Local Similarity 95.9%; Pred. No. 0;	

QY 1081 TAATATTGTCGACAAAGAACGGCGCAGTATATGCGATGCAAAACAGGTGCGTG 1140  
DB 1081 TAATATTGTCGATRAGAAGCGTGGCGAGTATATGCGATGCAAAACAGGTGCGTG 1140  
QY 1141 CGGTGCTCTCAGGTAGGGACCTGTTTCTTAGTGTCTATCCAGGTATGCAATGCGATT 1200  
DB 1141 TGGTGTCTCTCA-GTGGAGACTCGTTTCTTAGTGTCTATCCAGGTATGCAATGCGTT 1199  
QY 1201 TGGCATGCATGCAAAAGGAATGTTCCAGGCTCAGTGCACCTCAACACCCCGTGCCT 1260  
DB 1200 TGGCATGCATGCAAAAGGAATGTTCCAGGCTCAGTGCACCTCAACACCCCGTGCCT 1259  
QY 1261 GGAATTGAGCAGTCCGGCTCGGTGTATAGTACGATCGGCTCGGCGCGGTGTTCCGA 1320  
DB 1260 GAAATTGAGCAGTCCGGCTCGGTGTACAGTACGATCGGCTCGGCGCGGTGTTCCGA 1319  
QY 1321 AGCAAAAAGGTGGTGTTCGTTACCGACAAACATTTATCCACCTTGACATTTTCACCA 1380  
DB 1320 AGTAAAAAGGTGGTGTTCGTTACCGACAAACCTTTGATCCACCTTGATATTTTCACCA 1379  
QY 1381 CCTCTTCCCGCGAGAACAGCATTCGCGAAAATCTATCCTCGGCTACTATAGCAAG 1440  
DB 1380 CCTCTTCCCGCGAGAACAGCATTCGCGAAAATCTATCCTCGGCTACTATAGCAAG 1439  
QY 1441 ATAGTCTTTCGTATGGGACAAACCGTGTGGCGGAAACAAAGCTTCTCGGGCGTCCCTCAA 1500  
DB 1440 ATAGTCTTTCGTATGGGACAAACCGTGTGGCGGAAACAAAGCTTCTCGGGCGTCCCTCAA 1499  
QY 1501 TCGAGCTGTACCCCATCTCATTTGCCAGAGATACCAAGCATCGAAGTCGATCGGCAATGG 1560  
DB 1500 TCGAGCTGTACCCCATCTCATTTGCCAGAGATACCAAGCATCGAAGTCGATCGGCAATGG 1559  
QY 1561 TCCATTACCTCTTCATGCTCGGAGACCGGCGGAGTGGTCCCAACAGTCCCAACGAG 1620  
DB 1560 TCCATTACCTCTTCATGCTCGGAGACCGGCGGAGTGGTCCCAACAGTCCCAACGAG 1619  
QY 1621 GTACGACAAAATCTGTCTGGGACCAACTCGCGCAGCCTACGAGAACCGCGGGGCCCAA 1680  
DB 1620 GTACGACAAAATCTGTCTGGGACCAACTCGCGCAGCCTACGAGAACCGCGGGGCCCAA 1679  
QY 1681 GTCCAGAGCGGCGCAAGCTGCTGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAAGGA 1740  
DB 1680 GTCCAGAGCGGCGCAAGCTGCTGAGATCGAGTGGTCGAAGCAGCAGTATTTCCAAAGGA 1739  
QY 1741 GCTCGAGCGCGCTATGGGCTGAACGATCTCATCAGTGGTTCGCGCTCAGAACG 1800  
DB 1740 GCGCGAGCGCGCTATGGGCTGAACGATCTCATCAGTGGTTCGCGCTCAGAACG 1799  
QY 1801 CGGTTCAAGTGTGTTTCGTTGGAACGGAGACGCTTTAGTTTGAAGGGTATATG 1860  
DB 1800 CGGTTCAAGGTTGTTTCGTTGGAACGGAGACGCTTTAGTTTGAAGGGTATATG 1859  
QY 1861 GAAGGGCCATACGATCGGGTCAACAGAGTGTCTGCAAGATGTTGGTGTAGCTGGTGCCA 1920  
DB 1860 GAAGGGCCATACGATCGGGTCAACAGAGTGTCTGCAAGATGTTGGTGTAGCTGGTGCCA 1919  
QY 1921 GCAGCATAG 1929  
DB 1920 GCAGCATAG 1928

RESULT 5  
AAZ58387  
ID AAZ58387 standard; DNA; 1928 BP.  
XX  
AC AAZ58387;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Rhinocladiaella atrovirens amino polyol amine oxidase RAT011-C4 DNA.  
XX  
KW Amino polyol amine oxidase; funonisin; mycotoxin; transgenic plant;

KW detoxification; animal feed; silage; selectable marker; ds.  
XX Rhinocladiaella atrovirens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1928  
FT /tag= a  
FT /note= "contains introns"  
FT intron 739..811  
FT /tag= b  
FT intron 1134..1185  
FT /tag= c  
XX  
PN WO200004159-A1.  
XX  
XX 27-JAN-2000.  
XX  
XX 08-JUL-1999; 99WO-US15454.  
XX  
XX 15-JUL-1998; 98US-0092936.  
XX 21-MAY-1999; 99US-0135391.  
XX  
XX (PION-) PIONEER HI-BRED INT INC.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Duvick JP, Gilliam JT, Maddox JR;  
XX  
XX WPI: 2000-182425/16.  
XX P-PSDB; AAY58905.  
XX  
XX New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading funonisin or structurally related mycotoxin in processed  
PT grain or in silage  
PT  
XX  
PS Claim 1; Page 147-148; 154pp; English.  
XX  
XX The present sequence is that of an isolated nucleic acid,  
CC designated RAT011-C4, of Rhinocladiaella atrovirens isolate RAT011,  
CC which encodes an amino polyol amine oxidase (AAPO, see AAY58905)  
CC capable of degrading funonisin, its hydrolysis product AP1, and  
CC related mycotoxins. The DNA was obtained by PCR amplification of  
CC RAT011 mycelial DNA using primers based on AAPO of E. spinifera  
CC ATCC 74269. The invention provides AAY58900-05) of R. atrovirens and  
CC AAZ58383-87) and polypeptides (see AAY58900-05) of R. atrovirens and  
CC Exophiala spinifera. The polynucleotides are used to transform  
CC plant cells normally susceptible to Fusarium or other toxin-producing  
CC fungus infection. Transgenic plants can be regenerated from the  
CC transformed plant cells. Also provided are methods for expressing  
CC both AAPO and a funonisin-esterase in a transgenic plant, and for  
CC producing AAPO enzyme in prokaryotic and non-plant eukaryotic  
CC systems. Transgenic plants capable of degrading funonisin or of  
CC producing the degrading enzymes are provided. Methods for  
CC detoxification of grain, grain processing, silage, food crops and  
CC in animal feed and rumen microorganisms are also disclosed. AAPO  
CC polynucleotide is also useful as a selectable marker.  
XX  
SQ Sequence 1928 BP; 449 A; 528 C; 534 G; 417 T; 0 other;

Query Match 92.7%; Score 1789; DB 21; Length 1928;  
Best Local Similarity 95.8%; Pred. No. 0;  
Matches 1848; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

QY 1 ATGGCACTTGACCGAGCTACATCAATCCCAAGCTGCCCTCCCGACAGGGTATTC 60  
DB 1 ATGGCACTTGACCGAGCTACATCAATCCCAAGCTGCCCTCCCGACAGGGTATTC 60  
QY 61 CACATCGGCTAGGCCCAACGAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120  
DB 61 CACCTCGGCTAGGCCCAACGAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120  
QY 121 GAGCGTTTGGCGGTGACAGACCGAGCTACGAGAAACAGGTTGCCCAAGCATTCGCAAT 180  
DB 121 GAGCGTTTGGCGGTGACAGACCGAGCTACGAGAAACAGGTTGCCCAAGCATTCGCAAC 180





PN WO200004159-A1.  
XX 27-JAN-2000.  
XX 08-JUL-1999; 99WO-US15454.  
XX 15-JUL-1998; 98US-0092936.  
PR 21-MAY-1999; 99US-0135391.  
XX (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
PI Duwick JP, Gilliam JT, Maddox JR;  
XX WPI; 2000-182425/16.  
DR P-PSDB; AAY58903.  
XX New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading fumonisin or structurally related mycotoxin in processed  
PT grain or in silage  
XX  
PS Claim 1; Page 143-44; 154pp; English.  
XX  
CC The present sequence is that of an isolated nucleic acid,  
CC designated RAT011-Cl, of Rhinocladiaella atrovirens isolate RAT011,  
CC which encodes an amino polyol amine oxidase (APAO, see AAY58903)  
CC capable of degrading fumonisin, its hydrolysis product AP1, and  
CC related mycotoxins. The DNA was obtained by PCR amplification of  
CC RAT011 mycelial DNA using primers based on APAO of E. spinifera  
CC ATCC 74269. The invention provides APAO polynucleotides (see  
CC AAY58903-87) and polypeptides (see AAY58900-05) of R. atrovirens and  
CC Exophiala spinifera. The polynucleotides are used to transform  
CC plant cells normally susceptible to Fusarium or other toxin-producing  
CC fungus infection. Transgenic plants can be regenerated from the  
CC transformed plant cells. Also provided are methods for expressing  
CC both APAO and a fumonisin-esterase in a transgenic plant, and for  
CC producing APAO enzyme in prokaryotic and non-plant eukaryotic  
CC systems. Transgenic plants capable of degrading fumonisin or of  
CC producing the degrading enzymes are provided. Methods for  
CC detoxification of grain, grain processing, silage, food crops and  
CC in animal feed and rumen microorganisms are also disclosed. APAO  
CC polynucleotide is also useful as a selectable marker.  
XX  
SQ Sequence 1928 BP; 448 A; 530 C; 536 G; 414 T; 0 other;

Query Match 92.7%; Score 1787.4; DB 21; Length 1928;  
Best Local Similarity 95.7%; Pred No. 0;  
Matches 1847; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

QY 1 ATGGCACTTGACCGAGCTACATCAATCCCCAAACGCTCGCCTCCCGCAGCAGGGTATTCC 60  
DB 1 ATGGCACTTGACCGAGCTACATCAATCCCCAAACGCTCGCCTCCCGCAGCAGGGTATTCC 60  
QY 61 CACATCGCGGTAGGCCCAAAACGAGCGAGGTATGTGACAATAGCTGGACAGATGGACAA 120  
DB 61 CACGTCGGCGTAGGCCCAAAACGAGCGAGGTATGCGACAATAGCTGGACAGATGGACAA 120  
QY 121 GACGCTTTGGCGGTGACAGACCCAGCTTACGAGAAACAGGTTGCCAAGCAATTCGCCAAT 180  
DB 121 GACGCTTTGGCGGTGACAGACCCGCTTACGAGAAACAGGTTGCCAAGCAATTCGCCAAC 180  
QY 181 CTGCGAGCTTGCTGCTGCAGTGGAGCCCTTCAACACGAGCTCAGCAAGCTCAATTTAC 240  
DB 181 CTGCGAGCTTGCTGCTGCAGTGGAGCCACTTCAACAGCATATACCAAGCTCAATTTAC 240  
QY 241 TACATCGTCGACTAGCCCGGAGCAAACTACCGCAATTTGGAGATGGGCTGAAGCTTACC 300  
DB 241 TACATCGTCGACTACAAACCCGAGCAAACTACCGCAATTTGGAGATGGGCTGAAGGCTACC 300  
QY 301 TTTGCCCTTGACAGGCTCCCTTCTGACGCTGGTGCCAGTACCGGCGCTTGGCTTACCT 360  
DB 301 TTTGCCCTTGACAGGCTCCCTTCTTGCACGCTGGTGCCAGTACCGGCGCTTGGCTTACCT 360

QY 361 GAATACCTCTTTGAGCTTGATGCCACGGCGCTGGTCCAGGACACTCGACCCGACACAA 420  
DB 361 GAATACCTCTTTGAGCTTGATGCCACGGCGCTGGTTCAGGACACTCAACCCGACACAA 420  
QY 421 GTTGGCGAGCTGGTAGTGGTGGCGCTGGCTTGAGCGGTTTGGAGACGCGACGCAAAATC 480  
DB 421 GTTGGCGAGCTGGTAGTGGTGGCGCTGGCTTGAGCGGTTTGGAGACGCGACGCAAAATC 480  
QY 481 CAGGCGCGGCTGCTGCTCCCTCGCTTCTTGAGGCGATCGATCGTGTAGGGGGAAGACT 540  
DB 481 CAGGCTGCCGGGCTGCTCCCTCGCTTCTTGAGGCGATCGATCGTGTGGGGGAAGACT 540  
QY 541 CTGAGGCTACAATCGGGTCCCGGCGAGGAGCTATCAACGAGCTCGGCGCTCGCTGGATC 600  
DB 541 CTGAGGCTACAATCGGGTCCCGGCGAGGAGCTATCAATGACCTCGGCGCTCGCTGGATC 600  
QY 601 AATGACAGCAACCAAGCGAAGTATCCGATTTGTTTAAAGATTTTCAATTTGGAGGCGAG 660  
DB 601 AATGACAGCAACCAAGCGAAGTATTTCAAAATTTATTTGAAAGATTTTCAATTTGGAGGCGAG 660  
QY 661 CTCGAGGAGCAGCGGAAATTCATCCATCAGCACAGAGGCTACACCACTACAGCT 720  
DB 661 CTCGAGGAGCAGCGGAAATTCATCCATCAGCACAGAGGCTACACCACTACAGCT 720  
QY 721 CCTATGGTGACTCCCGGCTAAGCAAAATCCCACTTTGTGATGAGACCTCTCTCGAGTGT 780  
DB 721 CCTATGGTGATTCCTCGTGTAGCACAAATTCATCTTTGATGAGACCTCTCTCTGTGTGT 780  
QY 781 AGAATACAGTCACTACTCCACTTCCTCAGCTGAGCGAGGAGTTGCAAGTGCATTTGC 840  
DB 781 AGAATACAGTCACTACTCCACTTCCTCAGCTGAGCGAGGAGTTGCAAGTGCATTTGC 840  
QY 841 GGAACCTCTCCCGTATGCTCAGCTGATCGAAGAGTATAGCTTGAAGACCCCAAGC 900  
DB 841 GGAACCTCTCCCGATGCTCAGCTGATCGAAGAGCATAGTCTTGAAGACCCCAAGC 900  
QY 901 GAGCCCTCAGCGCAAGCGGCTGCACAGTGTGAGCTTCGCGCAGTACTGTGAGAAGGACT 960  
DB 901 GAGCCCTCAGCGCAAGCAGCTGCACAGTGTGAGCTTCGCGCAGTACTGTGAGAAGGACT 960  
QY 961 AAACCTTGCTGCTGCTCAGCTGCGCAACACAGATCACACGCGCTCTCTCGGTGTGA 1020  
DB 961 AAGCTTGCTGCTGCTGCTCGCGCTGGCAAAACAGATCACACGCGCTCTCTCGGTGTGA 1020  
QY 1021 AGCCACGAGATCAGCATGCTTTTCTCAGCGACTACATCAAGCTGCCAGTATATCGATGCAAAACAGGTCGCTG 1080  
DB 1021 AGCCACGAGATCAGCATGCTTTTCTCAGCGACTACATCAAGAGTGGCCAGGTCCTCAG 1080  
QY 1081 TAATATTGCTCGGACAAGAACGCGCGGAGTATATCGATGCAAAACAGGTCGCTG 1140  
DB 1081 TAATATTGCTCGGATTAAGAAAGCGGTGGCAGTATATCGATGCAAAACAGGTCGCTG 1140  
QY 1141 CGGTGCTCTCAGGTAGGAGACTCGTTCTTCTAGTGGTCAATTCAGGTATGAGTGCATT 1200  
DB 1141 TGGTGTCTCTCA - GTGGGAGACTCGTTCTTCTAGTGGTCAATTCAGGTATGAGTGCCTT 1199  
QY 1201 TGCCATGCCATGTCAAGGNACTTTGTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260  
DB 1200 TGCCATGCCATGTCAAGGNACTTTGTCAGGCTCAGTGCACCTCAACACCCCGCTCGCC 1259  
QY 1261 GGAATTTGAGCAGTCGGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCGCA 1320  
DB 1260 GAAATTTGAGCAGTCGGGCTCGGCTGTACGATGATCGGCTCGGCGCGCTGTTCGCA 1319  
QY 1321 AGCAAAAGTGGTGGTTTGGTTACCGACAACATTTGATCCCACCTTGACATTTTACCA 1380  
DB 1320 AGTAAAAAGTGGTGGTTTGGTTACCGACAACCTTGTATCCCACCTTGATATTTTACCA 1379  
QY 1381 CTTCTTCCCGCCGAGAGCAAGCAATTTGGCGGGAANAATCTATCCTCGGCTACTATAGCAAG 1440  
DB 1380 CTTCTTCCCGCCGAGAGCAAGCAATTTGGCTGAAAAATCCATCCTGCGGCTACTATAGCAAG 1439  
QY 1441 ATAGTCTTCTGATGGGACAACCGCTGGTGGCGGCAACAAAGGCTTCTCGGGCGCTTCCCAA 1500

|||||  
Db 1440 ATAGTCTTCGTATGGACAAGCCGTGGTGGCGGAACAAAGCCTTCTCGGGGCTCCTCAA 1499  
QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGATCGCAAGTCGATCGGCAATGG 1560  
Db 1500 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGATCGCAAGTCGATCGGCAATGG 1559  
QY 1561 TCCATTACCTGTTTCATGTCGGAGACCCGGGAGGAAAGTGGTCCCAACAGTCCCAAGCAG 1620  
Db 1560 TCCATTACCTGTTTCATGTCGGAGACCCGGGAGGAAAGTGGTCCCAACAGTCCCAAGCAG 1619  
QY 1621 GTACGACAAAAGTCTGTCTGGGACCACTCCGGCAGCCTACGAGAACGCCGGGGCCCAA 1680  
Db 1620 GTACGACAAAAGTCTGTCTGGAACCAACTCCGCGAGCCTACGAGAACGCCGGGGCCCAA 1679  
QY 1681 GTCCAGAGCCGGCCCAACGTCGTAATCGAGTGGTGGAGGACGAGTATTTCCAAAGGA 1740  
Db 1680 GTCCAGAGCCGGCCCAACGTCGAGATCGAGTGGTGGAGGACGAGTATTTCCAAAGGA 1739  
QY 1741 GTCGAGCGCGCTATATGGCTGAACGATCTCATACACTGGGTTCGGCGCTCAGAAGC 1800  
Db 1740 GCGCGAGCGTCTATATGGGTGAACGTCTCAACACACTGGGTTCGGCGCTCAGAAGC 1799  
QY 1801 CCGTTCAAGTGTGTTTCATTCTGTTGGAACGAGACGCTCTTTAGTTTGGAAAGGTATATG 1860  
Db 1800 CCGTTCAAGGTTGTTTCATTCTGTTGGAACGAGACGCTCTTTGGTTTGGAAAGGTATATG 1859  
QY 1861 GAAGGGGCATACGATCGGTTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGGCTGTGGCCA 1920  
Db 1860 GAAGGGGCATACGATCGGTTCAACGAGGCGCTCAGAGGCGCTGCAGAAAGTTGTGGCTAGGCTGTGGCCA 1919  
QY 1921 GCAGCATAG 1929  
Db 1920 GCAGCATAG 1928  
  
RESULT 7  
ID AA258402 standard; cDNA; 1803 BP.  
XX  
AC AA258402;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Exophiala spinifera amino polyol amine oxidase cDNA.  
XX  
KW Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;  
KW detoxification; animal feed; silage; selectable marker; ds.  
XX  
OS Exophiala spinifera.  
XX  
PN WO200004159-A1.  
XX  
PD 27-JAN-2000.  
XX  
PF 08-JUL-1999; 99WO-US15454.  
XX  
PR 15-JUL-1998; 98US-0092936.  
XX  
PR 21-MAY-1999; 99US-0135391.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
XX  
PI Duwick JP, Gilliam JT, Maddox JR;  
XX  
DR WPI; 2000-182425/16.  
DR P-PSDB; AAY58913.  
XX  
PT New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading fumonisin or structurally related mycotoxin in processed  
PT grain or in silage -  
XX  
PS Example 10; Page 97-100; 154pp; English.

XX The present sequence is that of the coding region of full-length  
CC amino polyol amine oxidase (APAO) cDNA of Exophiala spinifera  
CC 2141.10. APAO is capable of degrading fumonisin, its hydrolysis  
CC product APL, and related mycotoxins. The invention provides APAO  
CC polynucleotides (see AAY58383-87) and polypeptides (see AAY58900-05) of  
CC E. spinifera and Rhinocladiella atrovirens. The polynucleotides are  
CC used to transform plant cells normally susceptible to Fusarium or  
CC other toxin-producing fungus infection. Transgenic plants can be  
CC regenerated from the transformed plant cells. Also provided are  
CC methods for expressing both APAO and a fumonisin-esterase in a  
CC transgenic plant, and for producing APAO enzyme in prokaryotic and  
CC non-plant eukaryotic systems. Transgenic plants capable of degrading  
CC fumonisin or of producing the degrading enzymes are provided.  
CC Methods for detoxification of grain, grain processing, silage, food  
CC crops and in animal feed and rumen microorganisms are also disclosed.  
CC APAO polynucleotide is also useful as a selectable marker.  
XX  
SQ Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;  
  
Query Match 83.1%; Score 1602.6; DB 21; Length 1803;  
Best Local Similarity 91.7%; Pred. No. 0;  
Matches 1769; Conservative 0; Mismatches 34; Indels 126; Gaps 2;  
  
QY 1 ATGGCACTTGACCGAGCTACATCAATCCCCAAACGTCCCTCCCCAGCAGGTATTC 60  
Db 1 ATGGCACTTGACCGAGCTACATCAATCCCCAAACGTCCCTCCCCAGCAGGTATTC 60  
  
QY 61 CACATCGGCTAGCGCCCAACGAGGAGGTATGTACAAATAGCTGGACAGATTGACAA 120  
Db 61 CAGTCGGCTAGCGCCCAACGAGGAGGTATGTACAAATAGCTGGACAGATTGACAA 120  
  
QY 121 GACGCTTTTGGGCGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180  
Db 121 GACGCTTTGCGGCGTGACAGACCCCTGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180  
  
QY 181 CTGCGAGCTTGCCCTTGCTGAGTTGGAGCCTCTTCAAACGAGCTCAACAGCTCAATTAC 240  
Db 181 CTGCGAGCTTGCCCTTGCTGAGTTGGAGCCTCTTCAAACGAGCTCAACAGCTCAATTAC 240  
  
QY 241 TACATGTCGACTACGCCCGAGCAAACTCACCGCAATTTGGAGATGGCTGAAGTCTACC 300  
Db 241 TACATGTCGACTACGCCCGAGCAAACTCACCGCAATTTGGAGATGGCTGAAGTCTACC 300  
  
QY 301 TTTGCCCTTGACAGGCTCCCTCTTGCAGCTGGTGCCAGTACCGGCCCTTGGCTTCACCT 360  
Db 301 TTTGCCCTTGACAGGCTCCCTCTTGCAGCTGGTGCCAGTACCGGCCCTTGTCTTCACCT 360  
  
QY 361 GAATACCTCTTTGAGGTTGATGCCACGGGCTGGTGCCAGGACACTCGACCCAGACAAAC 420  
Db 361 GAATACCTCTTTGAGGTTGATGCCACGGGCTGGTGCCAGGACACTCGACCCAGACAAAC 420  
  
QY 421 GTATGCGAGCTGTAGTGGGCGCTGGCTTGAGCGGTTTGAGACGGCAGCGCAAGTC 480  
Db 421 GTTGGCGAGCTGTAGTGGGCGCTGGCTTGAGCGGTTTGAGACGGCAGCGCAAGTC 480  
  
QY 481 CAGGCGCGCGCTGTCTGCTCCCTCTTGTAGGGCATGGATCGTGTAGGGGAAAGACT 540  
Db 481 CAGGCGCGCGCTGTCTGCTCCCTCTTGTAGGGCATGGATCGTGTAGGGGAAAGACT 540  
  
QY 541 CTGAGCGTACATCGGGTCCCGGAGGAGCTATCAACAGCCTCGGCGCTCGTGGGATC 600  
Db 541 CTGAGCGTACATCGGGTCCCGGAGGAGCTATCAACAGCCTCGGCGCTCGTGGGATC 600  
  
QY 601 AATGACAGCAACCAAGGAAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGCGGAG 660  
Db 601 AATGACAGCAACCAAGGAAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGCGGAG 660  
  
QY 661 CTCAGAGGACGACCGGAAATTCATCCATCAAGCAACAGCGGTACAACTACTACAGCT 720  
Db 661 CTCAGAGGACGACTGAAATTCATCCATCAAGCAACAGCGGTACAACTACTACAGCT 720  
  
QY 721 CCTTATGGTGACTCCCGGTAAGCAACAATCCCACTTTGTGATGAGACCTCTGTGCGAGTGT 780

Db 721 ||||| 734  
CCTTATGGTGA

QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGGTGCAAGTGCACCTTGC 840  
|||

Db 735 -----CTTCTGAGCGAGGAGGTGCAAGTGCACCTTGC 767  
|||

QY 841 GGAACCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCCTTGAAGACCCCAAGGC 900  
|||

Db 768 GGAACCTCTCCCGTATGGTCTCAGCTGATCGAAGAGCATAGCCCTCAAGACCTCAAGGC 827  
|||

QY 901 GAGCCCTCAGGGGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT 960  
|||

Db 828 GAGCCCTCAGGGGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGAACT 887  
|||

QY 961 AAACCTTGCTGCTGTCTCAGCTGGCAAAACAGATCACACGCGCTCTGCTCGGTGTGGA 1020  
|||

Db 888 AAACCTTGCTGCTGTCTCGGCTAGCAACACAGATCACACGCGCTCTGCTCGGTGTGGA 947  
|||

QY 1021 AGCCACAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1080  
|||

Db 948 AGCCACAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1007  
|||

QY 1081 TAATATTTCTCGGACAGAAAGACGGCGGCGAGTATATGCGATGCAAAACAGGTGCGTG 1140  
|||

Db 1008 TAATATTTCTCGGACAGAAAGACGGCGGCGAGTATATGCGATGCAAAA----- 1057  
|||

QY 1141 CGGTGCTCTCAGTAGGGACTCGTTTCTTAGTGGTCAATCCAGGTATCAGTCGAT 1200  
|||

Db 1058 -----CAGGTATCAGTCGAT 1074  
|||

QY 1201 TGCCATGCCATGCAAGGAACCTTTTCCAGGCTCAGTGCACCTCAACACCCCGTGCCT 1260  
|||

Db 1075 TGCCATGCCATGCAAGGAACCTTTTCCAGGCTCAGTGCACCTCAACACCCCGTGCCT 1134  
|||

QY 1261 GGAATTGACAGTCCGGCTCGGCTGTATAGTACGATCGGCGCTCGGGCGCGGTGTCCGA 1320  
|||

Db 1135 GAAATTGACAGTCCGGCTCGGCTGTACAGTACGATCGGCGCTCGGGCGCGGTGTCCGA 1194  
|||

QY 1321 AGCAAAAGGTGGTGTTCGTTACCGACACATTTGATCCACCTTACACATTTTCACCA 1380  
|||

Db 1195 AGCAAAAGGTGGTGTTCGTTACCGACACCTTTGATCCACCTTACACATTTTCACCA 1254  
|||

QY 1381 CCTCTTCCGCGGAGAACGACATTTGGCGAAATAATATCTCTCGGCTACTATAGCAAG 1440  
|||

Db 1255 CCTCTTCCGCGGAGAACGACATTTGGCGAAATAATCTATCTCTGGGCTACTATAGCAAG 1314  
|||

QY 1441 ATAGTCTTGTATGGAGCAACCCGTGTGTGGCGGCGAACAAGGTTCTCGGGCGTCTCCAA 1500  
|||

Db 1315 ATAGTCTTGTATGGAGCAACCCGTGTGTGGCGGCGAACAAGGTTCTCGGGCGTCTCCAA 1374  
|||

QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACAGCATCGAGTCGATCGGCAATGG 1560  
|||

Db 1375 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACAGCATCGAGTCGATCGAACAATGG 1434  
|||

QY 1561 TCCATTACCTGTTTCATGGTCTGGAGACCGGAGAGTGTGTCACACAGTCCCAAGCAG 1620  
|||

Db 1435 TCCATTACCTGTTTCATGGTCTGGAGACCGGAGAGTGTGTCACACAGTCCCAAGCAG 1494  
|||

QY 1621 GTACGACAAAAGTCTGTCTGGACCAACTTCGCGGAGCCTACGAGACCGCGGGGCCCAA 1680  
|||

Db 1495 GTACGACAAAAGTCTGTCTGGACCAACTTCGCGGAGCCTACGAGACCGCGGGGCCCAA 1554  
|||

QY 1681 GTCCAGAGCCGCGGCTGCTGCAATCGAGTGGTCAAGCAGCATATTTCCAAGGA 1740  
|||

Db 1555 GTCCAGAGCCGCGGCTGCTGCAATCGAGTGGTCAAGCAGCATATTTCCAAGGA 1614  
|||

QY 1741 GTCCAGAGCCGCGGCTGCTGCAATCGAGTGGTCAAGCAGCATATTTCCAAGCAG 1800  
|||

Db 1615 GCTCCAGAGCCGCTATATGGGTGACAGTCTCATCATCTGAGTGGTTCGCGCTCAGAACG 1674  
|||

QY 1801 CCGTTCAAGTGTGTTCAATTCCTTGGACCGGAGAGCTCTTAGTTTGGAAAGGATATG 1860  
|||

Db 1675 CCGTTCAAGAGTCTTCATTTTCGTTGGAAGGAGACGCTTTAGTTTGAAGGGTATATG 1734  
|||

QY 1861 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAAGAAGTGTGTGCTAGCCTGGTGCCA 1920  
|||

Db 1735 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAAGAAGTGTGTGCTAGCCTGGTGCCA 1794  
|||

QY 1921 GCAGCATAG 1929  
|||

Db 1795 GCAGCATAG 1803  
|||

RESULT 8  
AAZ60641  
ID AAZ60641 standard; DNA; 1803 BP.  
XX  
AC AAZ60641;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE DNA encoding a full length aminopolyol amine oxidase APAO.  
XX  
KW Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;  
KW plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.  
XX  
OS Exophiala spinifera.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1803  
FT /tag= a  
FT /product= "aminopolyol amine oxidase"  
XX  
WO200004160-A1.  
XX  
PD 27-JAN-2000.  
XX  
PF 08-JUL-1999; 99WO-US15455.  
XX  
PR 15-JUL-1998; 98US-0092936.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
PI Crasta OR, Duwick J, Folkerts O, Gilliam JT, Maddox JR;  
XX  
XX WPI: 2000-182426/16.  
DR P-PSDB; AAY68849.  
XX  
PT New nucleic acid encoding aminopolyol amine oxidase, used, e.g. to  
PT generate plants resistant to Fusarium -  
XX  
PS Example 10; Page 99-101; 145pp; English.  
XX  
CC The present sequence encodes a full length Exophiala spinifera  
CC aminopolyol amine oxidase (APAO). The enzyme has homology to the  
CC flavin containing amine oxidase family, that oxidize primary amine  
CC to an aldehyde or ketone, releasing ammonia and hydrogen peroxide.  
CC The APAO enzyme degrades mycotoxins that promote fungal invasion of  
CC plants. Destruction of mycotoxins by APAO generates, as a by-product,  
CC hydrogen peroxide which is itself an antimicrobial and stimulates the  
CC plants own defensive systems. The APAO polynucleotides are used to  
CC generate plants (particularly maize) that are resistant to Fusarium or  
CC other fungi that produce mycotoxins and/or to degrade such mycotoxins  
CC (e.g. during ensiling); for recombinant production of APAO  
CC polypeptides; as selection markers for plant transformation; and to  
CC isolate related sequences from other organisms. The APAO polypeptides  
CC are used to degrade mycotoxins in plant materials, including expression  
CC in engineered bacteria and fungi, e.g. rumen microflora.  
XX  
SQ Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;

Query Match 83.1%; Score 1602.6; DB 21; Length 1803;  
Best Local Similarity 91.7%; Pred. No. 0;  
Matches 1769; Conservative 0; Mismatches 34; Indels 126; Gaps 2;

QY 1 ATGGCACTTGCACCGAGCTACATCAATCCCAAGAGTGCCTCCCAAGAGGGTATTCC 60  
DB 1 ATGGCACTTGCACCGAGCTACATCAATCCCAAGAGTGCCTCCCAAGAGGGTATTCT 60  
QY 61 CACATCGGCGTAGGCCCAACAGAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120  
DB 61 CACGTGCGGCTAGGCCCAACAGAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120  
QY 121 GAGCCTTTGGGCGTGACAGACCCAGCTACGAGAACAGGTTGCCAAGCAATCCCAAT 180  
DB 121 GAGCCTTTGGGCGTGACAGACCCAGCTACGAGAACAGGTTGCCAAGCAATCCCAAT 180  
QY 181 CTGCGAGCTTGCCCTGCTGCTCAGTTGAGGCTCTTCAACAGAGCTCACCAAGCTCAATTAC 240  
DB 181 CTGCGAGCTTGCCCTGCTGCTCAGTTGAGGCTCTTCAACAGAGCTCACCAAGCTCAATTAC 240  
QY 241 TACATCGTCGACTACGCCCGGAGCAACATCACGCCAATTTGGAGATGGGTGAAGCTTACC 300  
DB 241 TACATCGTCGACTACGCCCGGAGCAACATCACGCCAATTTGGAGATGGGTGAAGCTTACC 300  
QY 301 TTTGCCCTTTGACAGGCTCCCTCTTGCACGCTGGTGCCAGTACCGGCTTTGGCTTCACT 360  
DB 301 TTTGCCCTTTGACAGGCTCCCTCTTGCACGCTGGTGCCAGTACCGGCTTTGGCTTCACT 360  
QY 361 GAATACCTCTTTGAGGTTGATGCGACGGCGCTGGTGCCAGGACTTCGACGCCAGCTTAC 420  
DB 361 GAATACCTCTTTGAGGTTGATGCGACGGCGCTGGTGCCAGGACTTCGACGCCAGCTTAC 420  
QY 421 GTTGGCGAGCTGGTAGTGTGGGCGCTGGCTTTCGAGGAGTGGTGGAGACGGCAGCAAGTC 480  
DB 421 GTTGGCGAGCTGGTAGTGTGGGCGCTGGCTTTCGAGGAGTGGTGGAGACGGCAGCAAGTC 480  
QY 481 CAGGCGCGCGGCTGTCCTTCCTGAGGCGATGATCGTGTAGGGGGAAGACT 540  
DB 481 CAGGCGCGCGGCTGTCCTTCCTGAGGCGATGATCGTGTAGGGGGAAGACT 540  
QY 541 CTGAGGCTACATCGGCTCCCGGAGGAGGACTATCAAGGACTCGGGCTGCGTGGATC 600  
DB 541 CTGAGGCTACATCGGCTCCCGGAGGAGGACTATCAAGGACTCGGGCTGCGTGGATC 600  
QY 601 AATGACAGCAACCAAGCAAGTATCCAGATGTTTGAAGATTTCATTTGAGGCGCCAG 660  
DB 601 AATGACAGCAACCAAGCAAGTATCCAGATGTTTGAAGATTTCATTTGAGGCGCCAG 660  
QY 661 CTCGAGAGGACACCGGAAATTCATCCATCAAGCACAGAGCTACACCACTACAGCT 720  
DB 661 CTCGAGAGGACACTGGAAATTCATCCATCAAGCACAGAGCTACACCACTACAGCT 720  
QY 721 CCTTATGGTGACTCCCGGTAGCACATCCCACTTTGTGATGAGACCTCTGTCAGTGT 780  
DB 721 CCTTATGGTGACTCCCGGTAGCACATCCCACTTTGTGATGAGACCTCTGTCAGTGT 780  
QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGGTTGCAAGTGCATTGC 840  
DB 735 -----CTTGCTGAGCGAGGAGGTTGCAAGTGCATTGC 767  
QY 841 GGAAGTCTCCCGGTATGGTCTCAGCTGATGAGAGATATAGCCTTGAAGACCCCAAGC 900  
DB 768 GGAAGTCTCCCGGTATGGTCTCAGCTGATGAGAGCATAGCCTTCAAGACCTCAAGGC 827  
QY 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCCGCGCACTACTGTGAGAGGACT 960  
DB 828 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCCGCGCACTACTGTGAGAGGACT 887  
QY 961 AAACCTTGCCTGCTGCTCAGCTGGCAAAACAGATCACAGCGCTCTGCTCGGTGTGGA 1020  
DB 888 AAACCTTGCCTGCTGCTCAGCTGGCAAAACAGATCACAGCGCTCTGCTCGGTGTGGA 947  
QY 1021 AGCCACAGATCAGATGCTTTTCTCACCGACTTACATCAAGAGTGCACCGGTCTCAG 1080  
DB 948 AGCCACAGATCAGATGCTTTTCTCACCGACTTACATCAAGAGTGCACCGGTCTCAG 1007

QY 1081 TAATATTCTCGGACAAAGAGACGGCGCAGTATATGATGCAAAACAGGTGCGTG 1140  
DB 1008 TAATATTCTCGGACAAAGAGACGGCGCAGTATATGATGCAAAACAGGTGCGTG 1057  
QY 1141 CGGTGCTCTCAGGTAGGGACTCGTTTCTTAGTGTGTCATTCAGGTATGCAAGTATG 1200  
DB 1058 -----CAGGTATGCAAGTATG 1074  
QY 1201 TGCCATGCCATGTCAAAGGACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTGCCT 1260  
DB 1075 TGCCATGCCATGTCAAAGGACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTGCCT 1134  
QY 1261 GGAATTGAGCAGTCCGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA 1320  
DB 1135 GGAATTGAGCAGTCCGGCTCGGCTGTACAGTACGATCGGCTCGGCGCGCTGTTCCGA 1194  
QY 1321 AGCAAAAGGTGGTGTTCGTACCAGCAACATGTATCCCACTTTGACATTTTCAACA 1380  
DB 1195 AGCAAAAGGTGGTGTTCGTACCAGCAACCTGTATCCCACTTTGACATTTTCAACA 1254  
QY 1381 CCTCTTCCCGCGAGAAAGCAAGCATTCGGGAAATAATCTATCCTCGGCTACTATGCAAG 1440  
DB 1355 CCTCTTCCCGCGAGAAAGCAAGCATTCGGGAAATAATCTATCCTCGGCTACTATGCAAG 1314  
QY 1441 ATAGTCTTCGTATGGGACAAACCGTGTGGCGGAAAGGCTTCTCGGCGCTCTCCAA 1500  
DB 1315 ATAGTCTTCGTATGGGACAAACCGTGTGGCGGAAAGGCTTCTCGGCGCTCTCCAA 1374  
QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACAGCATCGAAGTCGATCGGCAATGG 1560  
DB 1375 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACAGCATCGAAGTCGATCGAATGG 1434  
QY 1561 TCCATTACCTGTTTCATGTCGGAGACCCGGGAGGAGTGTCCCAACAGTCCAAAGCAG 1620  
DB 1435 TCCATTACCTGTTTCATGTCGGAGACCCGGGAGGAGTGTCCCAACAGTCCAAAGCAG 1494  
QY 1621 GTACGACAAAGTCTGTCTGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGCCCCAA 1680  
DB 1495 GTACGACAAAGTCTGTCTGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGCCCCAA 1554  
QY 1681 GTCCACAGCGCGCAACGTCGCTCGAATCGAGTGTGCGAAGCAGCATTTTCCAAAGGA 1740  
DB 1555 GTCCACAGCGCGCAACGTCGCTCGAATCGAGTGTGCGAAGCAGCATTTTCCAAAGGA 1614  
QY 1741 GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATACACTGGGTCGGCGCTCAGAAGC 1800  
DB 1615 GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATACACTGGGTCGGCGCTCAGAAGC 1674  
QY 1801 CCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTTTTGTGGAAGGATATG 1860  
DB 1675 CCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTTTTGTGGAAGGATATG 1734  
QY 1861 GAAGGGCCATACGATCGGCTCAACGAGGTCGCAAGTTCGTGCTAGCCTGGTGCCA 1920  
DB 1735 GAAGGGCCATACGATCGGCTCAACGAGGTCGCAAGTTCGTGCTAGCCTGGTGCCA 1794  
QY 1921 GCAGCATAG 1929  
DB 1795 GCAGCATAG 1803

## RESULT 9

AAZ58407

ID AAZ58407 standard; cDNA; 2490 BP.

XX AAZ58407;

AC AAZ58407;

XX 23-MAY-2000 (first entry)

DT 23-MAY-2000 (first entry)

XX DNA encoding GST-truncated amino polyol amine oxidase fusion.

DE Amino polyol amine oxidase; APO; fumonisin; mycotoxin;

KW transgenic plant; detoxification; animal feed; silage;

KW

selectable marker; glutathione S transferase; GST; mutant; ss.

Chimeric - Schistosoma japonicum.  
Chimeric - Exophiala spinifera.  
Synthetic.

Key Location/Qualifiers

sig\_peptide 1..687  
/tag= a  
/product= "gst fusion + polylinker"

mat\_peptide 688..2076  
/tag= b  
/product= "K:trAPAO"

misc\_feature 688..690  
/tag= c  
/note= "extra lysine"

mutation replace(1288..1290, TCC)  
/tag= d

mutation replace(1303..1305, AAC)  
/tag= e

W0200004159-Al.

27-JAN-2000.

08-JUL-1999; 99WO-US15454.

15-JUL-1998; 98US-0092936.

21-MAY-1999; 99US-0135391.

(PION-) PIONEER HI-BRED INT INC.

(CURA-) CURAGEN CORP.

Duwick JP, Gilliam JT, Maddox JR;

WPI; 2000-182425/16.

P-PSDB; AAY58918.

New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage

Example 15; Page 131-135; 154pp; English.

The present sequence is that of a polynucleotide encoding a GST:APAO fusion protein (see AAY58918) composed of glutathione S transferase and Exophiala spinifera amino polyol amine oxidase (APAO). 2 Codons of the APAO coding region have been altered by site-directed mutagenesis in order to change the glycosylation pattern of the fusion protein. These were the replacement of AAT (Asn) by TCC (Ser) at codon 430, and replacement of AGC (Ser) by AAC (Asn) at codon 435. APAO is capable of degrading fumonisin and related mycotoxins. The invention provides APAO polynucleotides (see AAY58918) and polypeptides (see AAY58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants, prokaryotic and non-plant eukaryotic systems. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed.

Sequence 2490 BP; 625 A; 623 C; 653 G; 589 T; 0 other;

Query Match 82.7%; Score 1596.2; DB 21; Length 2490;  
Best Local Similarity 91.5%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;

QY 1 ATGGGCACTTGCACCGAGCTACATCAATCCCCCAACGTCGCTCCCCAGAGGGATTATCC 60

Db 688 ATGGCACTTGCACCGAGCTACATCAATCCCCCAACGTCGCTCCCCAGAGGGATTATCT 747

QY 61 CACATCGGCGTAGGGCCCAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120

Db 748 CACGTCGCGTAGGCCAGAGCGAGGAGGTATGTGACAATAGCTGGACAGATTGGACAA 807

QY 121 GACGCTTTGGCGGTGACAGAGCCACGCTACGAGAAACAGGTTGCCCAAGCAATTGCCCAAT 180

Db 808 GACGCTTCGGCGGTGACAGAGCCCTGCCTACGAGAAACAGGTTGCCCAAGCAATTGCCCAAT 867

QY 181 CTGCGAGCTTGCTTGCCTGTCAGTTGGAGCCTCTTCAAAACGAGCTCACCAAGCTCAATTAC 240

Db 868 CTGCGAGCTTGCTTGCCTGTCAGTTGGAGCCTCTTCAAAACGAGCTCACCAAGCTCAATTAC 927

QY 241 TACATCGTCGACTACGCCGCCGAGCAAACTCACCCCAATTGGAGATGGCTGAAGTCTAC 300

Db 928 TACATCGTCGACTACGCCGCCGAGCAAACTCACCCCAATTGGAGATGGCTGAAGTCTAC 987

QY 301 TTTGCCCTTGACAGGCTCCCTCTTGCAGCTGGTGGCAGTACCGGCTTGGCTTCACCT 360

Db 988 TTTGCCCTTGACAGGCTCCCTCTTGCAGCTGGTGGCAGTACCGGCTTGGCTTCACCT 1047

QY 361 GAATACCTCTTTGAGTTGATGCCACGGCGTGGTGCCAGGACACTCGACCCGACACAA 420

Db 1048 GAATACCTCTTTGAGTTGATGCCACGGCGTGGTGCCGAGACACAGCACCCGACAA 1107

QY 421 GTTGGGACCTGGTAGTGGTGGCGCTGGCTTGGAGCGGTTGGAGACGCGACGCAAGT 480

Db 1108 GTTGGGACCTGGTAGTGGTGGCGCTGGCTTGGAGCGGTTGGAGACGCGACGCAAGT 1167

QY 481 CAGGCCGCGGCTGTCTCTTGTAGGCGATGGATCGTGTAGGGGGAAGACT 540

Db 1168 CAGGCCGCGGCTGTCTCTTGTAGGCGATGGATCGTGTAGGGGGAAGACT 1227

QY 541 CTGAGCGTACAAATCGGCTCCGCGAGGAGCACTATCAAGACCTCGGCGCTCGCTGGATC 600

Db 1228 CTGAGCGTACAAATCGGCTCCGCGAGGAGCACTATCAAGACCTCGGCGCTCGCTGGATC 1287

QY 601 AATGACAGCAACAAAGCAAGTATCCAGATTGTTTGAAGATTTCATTGAGGCGCGAG 660

Db 1288 TCCGACAGCAACAAAGCAAGTATCCAGATTGTTTGAAGATTTCATTGAGGCGCGAG 1347

QY 661 CTCACAGAGCAGCCGAAATCAATCCATCAAGCAACAGCGGTACACCACTACAGCT 720

Db 1348 CTCACAGAGCAGCTGGAAATCAATCCATCAAGCAACAGCGGTACACCACTACAGCT 1407

QY 721 CTTATGTTGACTCCCGGCTAAGCAATCCCACTTTGTGTATGAGACCTCTCTGCGAGT 780

Db 1408 CTTATGTTGACTC----- 1421

QY 781 AGAATACAGTCACTGACTCCACTTCCTCAGCTGACGAGGAGGTTGCAAGTGCACCTTCG 840

Db 1422 -----CTTGCTGAGCGAGGAGTTGCAAGTGCACCTTCG 1454

QY 841 GGAACCTCTCCCGTATGGTCTCAGCTGATGGAAGAGTATAGCTTTGAAGACCCCAAGGC 900

Db 1455 GGAACCTCTCCCGTATGGTCTCAGCTGATGGAAGAGTATAGCTTTCAAGACCTCAAGGC 1514

QY 901 GAGCCCTCAGCGAAGCGGCTGCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGCACT 960

Db 1515 GAGCCCTCAGCGAAGCGGCTGCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGCACT 1574

QY 961 AAATTGCTGCTGTTCTCAGCGTGGCAACCAAGTACACGCGCTCTGCTCGGTGGA 1020

Db 1575 AAATTGCTGCTGTTCTCAGCGTGGCAACCAAGTACACGCGCTCTGCTCGGTGGA 1634

QY 1021 AGCCACGAGATCAGCATGCTTTTCTCAGCGTATCATCAAGAGTGCACCGGCTCTCAG 1080

Db 1635 AGCCACGAGATCAGCATGCTTTTCTCAGCGTATCATCAAGAGTGCACCGGCTCTCAG 1694

QY 1081 TAATATTGTCTCGACAAAGAAAGACGCGGCGAGTATATCGGATGCAAAACAGAGTCCGTG 1140

Db 1695 TAATATTGTCTCGACAAAGAAAGACGCGGCGAGTATATCGGATGCAAA----- 1744

QY 1141 CGGTGCTCTCTCAGGTAGGCGACTCGTTTCTTAGTGTCTATCCAGGTATGCACTGAT 1200



```
QY 241 TACATCGTCGACTAGCCGCCAGCAAACTCACCGCAATTGGAGATGGCTGAAGTCTACC 300
DB 928 TACATCGTCGACTAGCCGCCAGCAAACTCACCGCAATTGGAGATGGCTGAAGTCTACC 987
QY 301 TTGCGCCTTGACAGGCTCCCTCTCTTGACAGTGTGGTCCAGTACCGGCTTGGCTCACT 360
DB 988 TTGCGCCTTGACAGGCTCCCTCTCTTGACAGTGTGGTCCAGTGTGGCTTGTCTCACT 1047
QY 361 GAATACCTCTTTGAGGTGTGATSCCAGCGCTGTGGTCCAGGACACTCGACCCAGACAA 420
DB 1048 GAATACCTCTTTGAGGTGTGATSCCAGCGCTGTGGTCCAGGACACTCGACCCAGACAA 1107
QY 421 GTTGGGACGTGTAGTGTGGTGGCGCTGGCTTGAGCGTGTGGAGACGGCACGCAAGTGC 480
DB 1108 GTTGGGACGTGTAGTGTGGTGGCGCTGGCTTGAGCGTGTGGAGACGGCACGCAAGTGC 1167
QY 481 CAGGCGCGCGGTCTGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 1168 CAGGCGCGCGGTCTGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
QY 541 CTGAGCGTACAAATCGGGTCCCGGACGAGGACTATCAACGACCTCGCGCTGCGTGGATC 600
DB 1228 CTGAGCGTACAAATCGGGTCCCGGACGAGGACTATCAACGACCTCGCGCTGCGTGGATC 1287
QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCATTTGGAGGGCGAG 660
DB 1288 TCCGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCATTTGGAGGGCGAG 1347
QY 661 CTCAGAGGACGACCGGAAATCAATCATCAAGCACAAGACGCTACACACCTACAGCT 720
DB 1348 CTCAGAGGACGACCGGAAATCAATCATCAAGCACAAGACGCTACACACCTACAGCT 1407
QY 721 CTTATGCTGACTCCCGGTAAGCAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT 780
DB 1408 CTTATGCTGACTC----- 1421
QY 781 AGAATACAGTCACTGACTCCACTTGGTCCAGCTGAGCGAGGAGTTCGAAGTGCATTGC 840
DB 1422 -----CTTGCTGAGCGAGGAGTTCGAAGTGCATTGC 1454
QY 841 GGAACCTCTCCCGTATGCTCTGAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900
DB 1455 GGAACCTCTCCCGTATGCTCTGAGCTGATCGAAGAGTATAGCCTTGAAGACCTCAAGGC 1514
QY 901 GAGCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT 960
DB 1515 GAGCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACT 1574
QY 961 AAACCTGCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGA 1020
DB 1575 AAACCTGCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGA 1634
QY 1021 AGCCACAGATCAGCATGCTTTTCTCACGACTACATCAAGAGTGCACCGGCTCTCAG 1080
DB 1635 AGCCACAGATCAGCATGCTTTTCTCACGACTACATCAAGAGTGCACCGGCTCTCAG 1694
QY 1081 TAATATTCTCGGCAAGAAAGCGGCGGCAATATGCGATGCAAAACAGGTGCGGTG 1140
DB 1695 TAATATTCTCGGCAAGAAAGCGGCGGCAATATGCGATGCAAA----- 1744
QY 1141 CGGTGCTCTCAGTAGGGGACTGTTCTTAGTGTGCTATCCAGGTATGAGTGCAGT 1200
DB 1745 -----CAGGTATGAGTGCAGT 1761
QY 1201 TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTGGCT 1260
DB 1762 TGCCATGCCATGTCNAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTGGCT 1821
QY 1261 GSAATTGAGCAGTCGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA 1320
DB 1822 GAAATTGAGCAGTCGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA 1881
QY 1321 AGCAAAAAGGTGGTTCGTTTACCGCAACAATTTGATCCCACTTGACATTTTCACCA 1380
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DB 1882 AGCAAAAAGGTGGTTCGTTTACCGCAACCTTGTATCCCACTTGACATTTTCACCA 1941
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DB 1942 CCTTTCCTCCCGCAGAGCAAGCAATTGGCGAAAAATCTATCTCGGCTACTATAGCAAG 2001
QY 1441 ATAGTCTCTGATTTGGGACAAACCGTGGTGGCGGCAACAGGCTTCTCGGGCGTCTCCAA 1500
DB 2002 ATAGTCTCTGATTTGGGACAAACCGTGGTGGCGGCAACAGGCTTCTCGGGCGTCTCCAA 2061
QY 1501 TCGAGCTGTGACCCCTCTCATTTTGCAGAGATACCAAGCATCGAACTCGATCGGCAATGS 1560
DB 2062 TCGAGCTGTGACCCCTCTCATTTTGCAGAGATACCAAGCATCGATCGGCAATGS 2121
QY 1561 TCCATACCTGTTTCATGTCGAGACCCGGGACGGAAGTGTGTCCTCCCAAGTCCAAAGCAG 1620
DB 2122 TCCATACCTGTTTCATGTCGAGACCCGGGACGGAAGTGTGTCCTCCCAAGTCCAAAGCAG 2181
QY 1621 GTAGGACAAAGTCTGTCGGGACCAACTCCCGGCGACCTACGAGAACCGCGGGGCCAA 1680
DB 2182 GTAGGACAAAGTCTGTCGGGACCAACTCCCGGCGACCTACGAGAACCGCGGGGCCAA 2241
QY 1681 GTCCGAGAGCGGCCCAACGCTGCTCGAAATCGAGTGTGCAAGCAGCAGTATTTCCAAGGA 1740
DB 2242 GTCCGAGAGCGGCCCAACGCTGCTCGAAATCGAGTGTGCAAGCAGCAGTATTTCCAAGGA 2301
QY 1741 GTCGCGAGCGCGCTCATGAGGTGGAACGATCTCATCACACTGGGTTTCGGCGTCTAGAAGC 1800
DB 2302 GTCGCGAGCGCGCTCATGAGGTGGAACGATCTCATCACACTGGGTTTCGGCGTCTAGAAGC 2361
QY 1801 CCGTTCAAGTGTCTCATTTCCGTTGGAACGAGACCTCTTTAGTTTGGAAAGGTTATG 1860
DB 2362 CCGTTCAAGTGTCTCATTTCCGTTGGAACGAGACCTCTTTAGTTTGGAAAGGTTATG 2421
QY 1861 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAAGAGTGTGTCGCTAGCCTGCTGCCA 1920
DB 2422 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAAGAGTGTGTCGCTAGCCTGCTGCCA 2481
QY 1921 GCAGCATAG 1929
DB 2482 GCAGCATAG 2490
RESULT 11
AAZ58393
ID AAZ58393 standard; cDNA; 1442 bp.
XX
AC AAZ58393;
XX AC
DT 23-MAY-2000 (first entry)
XX
DE Amino polyol amine oxidase truncated DNA k0n0-395_5.4.
XX Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; ss.
XX Exophiala spinifera.
XX
FH Key Location/Qualifiers
FT CDS 1..1442
FT /tag= a
FT /note= "contains an intron"
FT intron 647..699
FT /tag= b
XX
PN WO200004159-A1.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15454.
XX
XX 15-JUL-1998; 98US-0092936.
```







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XX AAZ60631;
AC
XX
XX
DT 16-MAY-2000 (first entry)
XX
XX
DE DNA encoding an aminopolyol amine oxidase clone trAPAO-I.
XX
KW Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
KW plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
XX
OS Exophiala spinifera.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..1442
FT     /*tag= a
FT     /product= "aminopolyol amine oxidase"
FT     /note= "contains an intron"
FT exon 1..646
FT     /*tag= b
FT     /number= 1
FT intron 647..699
FT     /*tag= c
FT     /number= 1
FT exon 700..1439
FT     /*tag= d
FT     /number= 2
XX
PN WO200004160-A1.
XX
PD 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15455.
XX
PR 15-JUL-1998; 98US-0092936.
XX
PA (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
XX
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;
XX
XX WPI: 2000-182426/16.
DR P-PSDB; RAY68844.
XX
XX New nucleic acid encoding aminopolyol amine oxidase, used, e.g. to
XX generate plants resistant to Fusarium
XX
XX Example 6; Page 78-80; 145pp; English.
XX
XX The present sequence encodes an Exophiala spinifera aminopolyol amine
XX oxidase (APAO). The enzyme has homology to the flavin containing amine
XX oxidase family, that oxidise primary amine to an aldehyde or ketone,
XX releasing ammonia and hydrogen peroxide. The APAO enzyme degrades
XX mycotoxins that promote fungal invasion of plants. Destruction of
XX mycotoxins by APAO generates, as a by-product, hydrogen peroxide which
XX is itself an antimicrobial and stimulates the plants own defensive
XX systems. The APAO polynucleotides are used to generate plants
XX (particularly maize) that are resistant to Fusarium or other fungi
XX that produce mycotoxins and/or to degrade such mycotoxins (e.g. during
XX ensilaging); for recombinant production of APAO polypeptides; as
XX selection markers for plant transformation; and to isolate related
XX sequences from other organisms. The APAO polypeptides are used to
XX degrade mycotoxins in plant materials, including expression in
XX engineered bacteria and fungi, e.g. rumen microflora.
XX
XX Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
XX
XX Query Match 68.4%; Score 1319; DB 21; Length 1442;
XX Best Local Similarity 93.5%; Pred. No. 0;
XX Matches 1417; Conservative 0; Mismatches 25; Indels 73; Gaps 1;
XX
XX 415 GACAACGTTGGGACGTGGTAGTGGTGGCGCTGGCTTGAGCGGTTTGAGACGGCAGCG 474
XX |
XX 1 GACAACGTTGGGACGTGGTAGTGGTGGCGCTGGCTTGAGCGGTTTGAGACGGCAGCG 60
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QY 475 AAAGTCCAGGCCCGCGGTCTGTCTCCTGCTGTTCTTTGAGCGGATGATGCTGTAGGGGA 534
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Db 61 AAAGTCCAGGCCCGCGGTCTGTCTCCTGCTGTTCTTTGAGCGGATGATGCTGTAGGGGA 120
|
|
|
QY 535 AAGACTCTGAGCGGTACAAATCGGGTCCGGCAGGACCACTATCAACGACCTCGCGCGTGG 594
|
|
|
Db 121 AAGACTCTGAGCGGTACAAATCGGGTCCGGCAGGACCACTATCAACGACCTCGCGCGTGG 180
|
|
|
QY 595 TGGATCAATGACAGCAACCAAGCGAAGTATCCAGATTTGTTGAAAGATTTTCATTTGGAG 654
|
|
|
Db 181 TGGATCAATGACAGCAACCAAGCGAAGTATCCAGATTTGTTGAAAGATTTTCATTTGGAG 240
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QY 655 GCGAGCTCCAGAGGACGACCGGAAATTCATCCATCAAGCAACGAGCGGTACAACCACT 714
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Db 241 GCGAGCTCCAGAGGACGACGTGAAATTCATCCATCAAGCAACGAGCGGTACAACCACT 300
|
|
|
QY 715 ACAGCTCCTTATGCTGACTCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTC 774
|
|
|
Db 301 ACAGCTCCTTATGCTGACTC----- 320
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|
|
QY 775 GAGTGTAGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGGTTGCAAGTGC 834
|
|
|
Db 321 -----CTTGCTGAGCGAGGAGGTTGCAAGTGC 347
|
|
|
QY 835 ACTTGGGAACTCCTCCCGTATGTCTCAGTGTGGAAGAGTATAGCCTTTGAAGACCC 894
|
|
|
Db 348 ACTTGGGAACTCCTCCCGTATGTCTCAGTGTGGAAGAGTATAGCCTTTGAAGAA 407
|
|
|
QY 895 CAAGCGAGCCCTCAGCGAAGCGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAA 954
|
|
|
Db 408 CAAGCGAGCCCTCAGCGAAGCGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAA 467
|
|
|
QY 955 GGACCTAAACTTGCCTGCTGTTCTCAGCGTGGCAACCAAGATCACACGCGCTCTGCTCGG 1014
|
|
|
Db 468 GGAACCTAAACTTGCCTGCTGTTCTCGCGGTAGCAAAACAGATCACACGCGCTCTGCTCGG 527
|
|
|
QY 1015 TGTGGAAGCCCGACGATCAGCATGCTTTTCTCACCAGCTACATCAAGAGTGCACCGG 1074
|
|
|
Db 528 TGTGGAAGCCCGACGATCAGCATGCTTTTCTCACCAGCTACATCAAGAGTGCACCGG 587
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|
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QY 1075 TCTCAGTAATATGTCTCGGACAAGAACGCGCGGAGTATATGCGATGCAAAACAGG 1134
|
|
|
Db 588 TCTCAGTAATATTTCTCGGACAAGAACGCGCGGAGTATGTCGATGCAAAACAGG 647
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|
|
QY 1135 TGGTCCGCTGCTCTCAGGTGGGGACTCGTTTCTTCTCAGTGGTCAATCCAGGTATGCAG 1194
|
|
|
Db 648 TGGTCCGCTGCTCTCAGGTGGGGACTCGTTTCTTCTCAGTGGTCAATCCAGGTATGCAG 707
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QY 1195 TCGATTGGCCATGCCATGTCAAGGAACTTGTCCAGGCTCAGTGCACCTCAACACCGCC 1254
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|
Db 708 TCGATTGGCCATGCCATGTCAAGGAACTTGTCCAGGCTCAGTGCACCTCAACACCGCC 767
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|
QY 1255 GTCGCTGGAATTTGAGCAGTCCGCGTCTATAGTACGATCGGCTTCGGCGCCCGTG 1314
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Db 768 GTCGCTGGAATTTGAGCAGTCCGCTCTAGTACGATCGGCTTCGGCGCCCGTG 827
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QY 1315 TTCGGAAGCAAAAGTGGTGGTTTCGTTTACCGACAACATTTATCCACCTTTGACATTT 1374
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Db 828 TTCGGAAGCAAAAGTGGTGGTTTCGTTTACCGACAACCTTTATCCACCTTTGACATTT 887
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QY 1375 TCACCACCTTTCCCGCCGAGAGCAAGCATTTGGCGGAAAAATCTATCCTCGGCTACTAT 1434
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Db 888 TCACCACCTTTCCCGCCGAGAGCAAGCATTTGGCGGAAAAATCTATCCTCGGCTACTAT 947
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QY 1435 AGCAAGATAGTCTTCGTATGGGACAACCCGTTGGCGGCAACAGGCTTCTCGGGCGTC 1494
|
|
|
Db 948 AGCAAGATAGTCTTCGTATGGGACAACCCGTTGGCGGCAACAGGCTTCTCGGGCGTC 1007
|
|
|
QY 1495 CTCGAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCGATCGAAGTGCATCGG 1554
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|
|
Db 1008 CTCGAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCGATCGAGCTCGATCGA 1067
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Db 2109 GCTCGGTGTGAAGCCACAGATCAGCATGCTTTTCTCACGACTACATCAAGAGTC 2168  
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Db 2169 CACCGGTCTCAGTAATATTTCTCGGACAAGAGCGCGGCAGTATATGCGATGCAA 2228  
Qy 1129 AACAGGTGCGTGGGTCTCTCTCAGTAGGGGACTCGTTTCTTAGTGGTTCATCCAGGT 1188  
Db 2229 AA-----CAGGT 2235  
Qy 1189 ATGCAAGTCGATTTGCCATGCCATGTCAAAGGAACCTTTTCCAGGCTCAGTGCACTCAAC 1248  
Db 2236 ATGCAAGTCGATTTGCCATGCCATGTCAAAGGAACCTTTTCCAGGCTCAGTGCACTCAAC 2295  
Qy 1249 ACCCGGTCGCTGGAATTAGCAGTCCGGCTCGGCTGTATAGATCGCGGCTCGGGC 1308  
Db 2296 ACCCGGTCGCTGGAATTAGCAGTCCGGCTCGGCTGTATAGATCGCGGCTCGGGC 2355  
Qy 1309 GCGGTGTCGGAAGCAAAAGGTGCTTTCGTTACCGACAACATTTGATCCACCTTG 1368  
Db 2356 GCGGTGTCGGAAGCAAAAGGTGCTTTCGTTACCGACAACCTTTGATCCACCTTG 2415  
Qy 1369 ACATTTTACCACCTCTTCCGCGGAGAGCAAGCATTTGGCGAAATAATCTATCCTCGG 1428  
Db 2416 ACATTTTACCACCTCTTCCGCGGAGAGCAAGCATTTGGCGAAATAATCTATCCTCGG 2475  
Qy 1429 TACTATAGCAAGATAGTCTTCGTATGGGACAACCCGTTGGTGGCGGCAAGAGCTTCTCG 1488  
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Qy 1489 GCGTCTCCCAATCGAGTGTGACCCCATCTCATTTCCAGAGATACAGCATCGAAGTC 1548  
Db 2536 GCGTCTCCCAATCGAGTGTGACCCCATCTCATTTCCAGAGATACAGCATCGAAGTC 2595  
Qy 1549 GATCGCAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGTGCCAA 1608  
Db 2596 GATCGCAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGTGCCAA 2655  
Qy 1609 CAGTCCAGCAGGTACGCAAAAGTCTGTCTGGGACCACTCCGCGAGCTTACGAGAAC 1668  
Db 2656 CAGTCCAGCAGGTACGCAAAAGTCTGTCTGGGACCACTCCGCGAGCTTACGAGAAC 2715  
Qy 1669 GCGGGGCCAAGTCCAGAGCCGCAAGCTGCTCGAAATCGAGTGGTTCGAAAGCAGAG 1728  
Db 2716 GCGGGGCCAAGTCCAGAGCCGCAAGCTGCTCGAAATCGAGTGGTTCGAAAGCAGAG 2775  
Qy 1729 TATTTCCAGGAGTCCGAGCCGCTCTATGGGCTGAACGATCTCATCACTGGGTTCG 1788  
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Qy 1789 GCGTCCAGACCGCGTTCAGTGTTCATTTCTTGGAGCGAGAGCTCTTAGTTGG 1848  
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Qy 1849 AAAGGTATATGAAGGGCCATACGATCGGGTCAACGAGTGTCTGCAAGAGTGTGGCT 1908  
Db 2896 AAAGGTATATGAAGGGCCATACGATCGGGTCAACGAGTGTCTGCAAGAGTGTGGCT 2955  
Qy 1909 AGCCTGGTCCAGCAGCATAG 1929  
Db 2956 AGCCTGGTCCAGCAGCATAG 2976

RESULT 14

AZ60643  
ID AZ60643 standard; DNA; 2976 BP.  
XX AZ60643;  
AC  
XX  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE DNA encoding a fusion of aminopolylol amine oxidase/fumonisin esterase.

XX Aminopolylol amine oxidase; APAO; mycotoxin degradation; antimicrobial;  
KW plant fungal invasion; hydrogen peroxide; Fusarium; fungi;  
KW fumonisin esterase; ss.  
XX Synthetic.  
OS Exophiala spinifera.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2976  
FT /\*tag= a  
FT /product= "aminopolylol amine oxidase/fumonisin  
FT ester fusion"  
FT sig\_peptide 1..72  
FT /\*tag= b  
FT /note= "barley alpha amylase signal sequence"  
FT mat\_peptide 73..1545  
FT /\*tag= c  
FT /product= "fumonisin esterase"  
FT /note= "bacterial fumonisin esterase"  
FT misc\_feature 1546..1584  
FT /\*tag= d  
FT /note= "spacer sequence"  
FT mat\_peptide 1585..2973  
FT /\*tag= e  
FT /product= "aminopolylol amine oxidase"  
FT /note= "the protein has an amino terminal Lys  
FT for optimized expression"  
XX WO200004160-A1.  
XX 27-JAN-2000.  
XX  
XX 08-JUL-1999; 99WO-US15455.  
XX 15-JUL-1998; 98US-0092936.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX (CURA-) CURAGEN CORP.  
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;  
XX WPI; 2000-182426/16.  
XX P-PSDB; AAY68851.  
XX New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to  
XX generate plants resistant to Fusarium -  
XX Claim 14; Page 103-108; 145pp; English.  
XX The present sequence encodes a fusion protein of Exophiala spinifera  
XX aminopolylol amine oxidase (APAO) and a bacterial fumonisin esterase.  
XX The APAO enzyme has homology to the flavin containing amine oxidase  
XX family, that oxidise primary amine to an aldehyde or ketone, releasing  
XX ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins  
XX that promote fungal invasion of plants. Destruction of mycotoxins by  
XX antimicrobial and stimulates the plants own defensive systems. The  
XX APAO polynucleotides are used to generate plants (particularly maize)  
XX that are resistant to Fusarium or other fungi that produce mycotoxins  
XX and/or to degrade such mycotoxins (e.g. during ensiling); for  
XX recombinant production of APAO polypeptides; as selection markers for  
XX plant transformation; and to isolate related sequences from other  
XX organisms. The APAO polypeptides are used to degrade mycotoxins in  
XX plant materials, including expression in engineered bacteria and fungi,  
XX e.g. rumen microflora.

XX Sequence 2976 BP; 564 A; 932 C; 926 G; 554 T; 0 other;

Query Match 62.8%; Score 1212.2; DB 21; Length 2976;

Best Local Similarity 90.2%; Pred. No. 0;

Matches 1372; Conservative 0; Mismatches 23; Indels 126; Gaps 2;



PI Duwick JP, Gilliam JT, Maddox JR;

XX WPI: 2000-182425/16.

DR P-PSDB; AAY58914.

XX

PT New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading fumonisin or structurally related mycotoxin in processed  
PT grain or in silage

XX

XX Example 13; Page 102-106; 154pp; English.

XX

CC The present sequence is that of a polynucleotide encoding a  
CC fusion protein (see AAY58914) composed of the barley alpha-amylase  
CC signal peptide, and Exophiala spinifera fumonisin esterase (ESP1).  
CC joined via a peptide linker to k:trAPAO (see AAY58909), a truncated,  
CC but functional, amino polyol amine oxidase of E. spinifera. The  
CC construct was designed for expression and secretion in plants of a  
CC hybrid protein having ESP1 and APAO activity. The invention  
CC provides APAO polynucleotides (see AAY58383-87) and polypeptides (see  
CC AAY58900-05) of E. spinifera and Rhinocladia atraovirens. The  
CC polynucleotides are used to transform plant cells normally  
CC susceptible to Fusarium or other toxin-producing fungus infection.  
CC Also provided are methods for expressing APAO, optionally as a  
CC fusion protein with fumonisin esterase, in transgenic plants,  
CC prokaryotic and non-plant eukaryotic systems. Methods for  
CC detoxification of grain, grain processing, silage, food crops and  
CC in animal feed and rumen microorganisms are also disclosed.

XX

SQ Sequence 3003 BP; 690 A; 840 G; 819 G; 654 T; 0 other;

Query Match. 62.8%; Score 1212.2; DB 21; Length 3003;

Best Local Similarity 90.2%; Pred. No. 0;

Matches 1372; Conservative 0; Mismatches 23; Indels 126; Gaps 2;

QY 409 ACCCCAGACACGTTGGGACGTGGTAGTGGTGGGCGCTGGCTTGGAGACG 468

DB 1609 AGCAAGACACGTTGGGACGTGGTAGTGGTGGGCGCTGGCTTGGAGACG 1668

QY 469 GCAGCAAGTCCAGGCGCGGGTCTGCTGCTGCTGCTGCTGAGGCGATGGATGTA 528

DB 1609 GCAGCAAGTCCAGGCGCGGGTCTGCTGCTGCTGCTGCTGAGGCGATGGATGTA 1728

QY 529 GGGGGAAGACTCTGAGCGTACAATCGGGTCCCGGACGAGCGACTATCAACGACCTCGGC 588

DB 1729 GGGGGAAGACTCTGAGCGTACAATCGGGTCCCGGACGAGCGACTATCAACGACCTCGGC 1788

QY 589 GCTGGTGGATCAATGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAGATTTCAT 648

DB 1789 GCTGGTGGATCAATGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAGATTTCAT 1848

QY 649 TTGGAGGCGAGCTCCAGAGCAGCAGCGAATTCATCCATCAAGCACAAGCGGTACA 708

DB 1849 TTGGAGGCGAGCTCCAGAGCAGCAGCTGGAAATTCATCCATCAAGCACAAGCGGTACA 1908

QY 709 ACCACTACAGCTCCTTATGTTGACTCCCGGTAAGACAAATCCCACTTTGTGATGAGACC 768

DB 1909 ACCACTACAGCTCCTTATGTTGACTC-----CTTGCTGAGGAGGTTGC 828

QY 829 AAGTCACCTTGGGAACCTCCCGGTATGTTCTCAGCTGATCGAAGAGTATAGCCTTGA 888

DB 1956 AAGTCACCTTGGGAACCTCCCGGTATGTTCTCAGCTGATCGAAGAGTATAGCCTTGA 2015

QY 889 AGACCCCAAGGCGAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTG 948

DB 2016 AGACCTCAAGGCGAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTG 2075

QY 949 TGAGAGGACCTAAACTTGCCTGCTGTTCTCAGCGTGGCAACCAACAGATCACACGCGCTCT 1008

DB 2076 TGAGAGGAACTAAACTTGCCTGCTGTTCTCGGCGTAGCAAAACCAACAGATCACACGCGCTCT 2135

Search completed: November 12, 2002, 03:18:40

Job time : 441 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: November 12, 2002, 02:21:50 ; Search time 2809 seconds  
(without alignments)  
11121.785 Million cell updates/sec

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Perfect score: 1929  
Sequence: 1 atggcactgcaccagcta.....gctgtgcagcagcatag 1929

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_estli:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
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20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
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C 1	58.8	3.0	729 13	BJ375584 BJ375584
C 2	58.8	3.0	742 13	BJ341279 BJ341279
C 3	57.8	3.0	711 13	BJ373006 BJ373006
C 4	57.4	3.0	730 13	BJ377633 BJ377633
C 5	57.2	3.0	610 13	BJ431313 BJ431313
C 6	57.2	3.0	611 13	BJ374786 BJ374786

C 7	57.2	3.0	612 13	BJ428963
C 8	57.2	3.0	635 13	BJ399347
C 9	57.2	3.0	648 13	BJ375424
C 10	57.2	3.0	650 13	BJ375565
C 11	57.2	3.0	651 13	BJ372067
C 12	57.2	3.0	658 13	BJ430839
C 13	57.2	3.0	686 13	BJ374842
C 14	57.2	3.0	687 13	BJ429162
C 15	57.2	3.0	694 13	BJ375168
C 16	57.2	3.0	701 13	BJ398900
C 17	57.2	3.0	705 13	BJ372912
C 18	57.2	3.0	709 13	BJ375461
C 19	57.2	3.0	716 13	BJ429814
C 20	57.2	3.0	716 13	BJ435702
C 21	57.2	3.0	718 13	BJ375135
C 22	57.2	3.0	719 13	BJ374125
C 23	57.2	3.0	721 13	BJ375330
C 24	57.2	3.0	721 13	BJ435141
C 25	57.2	3.0	723 13	BJ374081
C 26	57.2	3.0	723 13	BJ430290
C 27	57.2	3.0	728 13	BJ401197
C 28	57.2	3.0	734 13	BJ375460
C 29	57.2	3.0	734 13	BJ431186
C 30	56.8	2.9	737 13	BJ375430
C 31	56.6	2.9	699 13	BJ434208
C 32	55.6	2.9	688 13	BJ346068
C 33	55.6	2.9	741 13	BJ400000
C 34	55	2.9	639 9	AU034174
C 35	50.4	2.6	278 13	BJ430253
C 36	49	2.5	573 13	BM180292
C 37	47.6	2.5	410 13	BJ374217
C 38	46.8	2.4	699 13	BJ377200
C 39	46.8	2.4	701 13	BJ402162
C 40	46.4	2.4	393 9	AU039258
C 41	46.4	2.4	566 9	AU034499
C 42	46.4	2.4	581 14	C22948
C 43	46.4	2.4	588 13	BJ434223
C 44	46.4	2.4	647 9	AU052223
C 45	46.4	2.4	737 13	BJ376587

ALIGNMENTS

RESULT 1  
LOCUS BJ375584/C  
DEFINITION BJ375584 Dictyostelium ddc19a09 3', mRNA sequence.  
ACCESSION BJ375584  
VERSION BJ375584.1 GI:19284967  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum.  
ORGANISM Dictyostelium discoideum  
REFERENCE 1 (bases 1 to 729)  
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
TITLE Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.  
stage Full length cDNA of Dictyostelium discoideum at the culmination

Unpublished (2002)  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
Location/Qualifiers  
1..729  
/organism="Dictyostelium discoideum"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="ddc19a09"

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/clone_lib="Dictyostelium discoideum cDNA library, CF"
/sex="mat A"
/dev_stage="Culmination stage"
BASE COUNT      214 a   136 c   129 g   250 t
ORIGIN

Query Match      3.0%; Score 58.8; DB 13; Length 729;
Best Local Similarity 44.3%; Pred. No. 1.5e-05;
Matches 295; Conservative 0; Mismatches 362; Indels 9; Gaps 1;

QY 1244 TCAACACCCCGCTGCGTGAATTCAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCT 1303
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 712  TAAATGCACAGGCGCTCCATATTTCAGATGCCAATCAATGACCAATTAACACTGATA 653
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1304 CGGCGCCCGCTGTTCCGAAGCAAAAGGTGGTGTTCGTTACCGACAACATGTTATCCCA 1363
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 652  ACGGTTCAACTTATCGTTCAAAATACATGTTGTTGCAATTCACCACATTTGGCTGGCC 593
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1364 CTTTGACATTTTCACCACTCTTCCGCGGAGAGAACGATGGCGGAAATCTATCC 1423
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 592  GTATTCAATTATCAACATCTATGCCACCAAGACGTGATGAACCTCAAAAGATGCCAA 533
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1424 TCGGCTACTATAGCAAGATGTTCTGATGGACAACCCGTTGGCGGCAACAAAGCT 1483
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 532  TGGGTTCCGTCATTAACCAATCACCATCTATGATGAACCATCTGGAGAAAGAGGTT 473
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1484 TPCGCGGCTCCTCCAACTCGAGCTGTGACCCCATCTCAATTTGCCAGAGATACCAATCG 1543
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 472  ATTCACTGAAGCCATCTGTATAAGGTCCTCAATCTTTATCTGCTATGATGACTCTTCAC 413
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1544 AGTCGATCGCAATGGTCCATTAACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGT 1603
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 412  ATGACGATGAAGAAACAGCATTTGTTGGTTTCATTTGCTGCTTCAGCCGCTAAAGATTGG 353
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1604 CCCAAGCTCCAAAGAGTACGACAAAGTCTGCTGGCAACCACTCCGCGCAGCTACG 1663
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 352  CTGAAAAATCACCAGAGAAAGAGAGCGCTCTAGACTGTTATGCTGTTGGTGGG 293
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1664 AGAACCCGGGCGCAAGTCCAGAGCGCGCAACGTCGTCGAAATCGAGTGGTGAAGC 1723
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 292  -----GTCCAAAGCATTTATCTCCAAGAAATCTTTTAGAGAAAAGTTGGAAGAAG 242
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1724 AGCAGTATTTCGAAGAGCTCCGAGCGCGCTATGCGCTGAACGATCTCATCACTGG 1783
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241  AGAATATTCAGTGGTGTATTAGTTACACTAGTCCAGGTAATCTCTACCAATGTG 182
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1784 GTCCGCGCTCAGAACCGCGTTCAAGTGTGTTTCATTTGGAACGGAGACGCTTTAG 1843
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181  GTGAACATTTACGTGCTCCAGTTGGTAGAATTCATTGGGCTGGTACAAACTGCTTCAG 122
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1844 TTTGGAAGGTTATATGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTG 1903
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121  TTTGGATTGGTTATATGAAGGTGCTTAGAATCAGGTTTATAGAGTTTCAAAAGAAATTA 62
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1904 TGGCTA 1909
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61  AAGATA 56
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
LOCUS      BJ341279/c
DEFINITION BJ341279 Dictyostelium discoideum cDNA library, AF Dictyostelium
           discoideum cDNA clone dda6b01 3', mRNA sequence.
ACCESSION  BJ341279
VERSION     BJ341279.1 GI:19249641
KEYWORDS   EST.
SOURCE      Dictyostelium discoideum.
            Dictyostelium discoideum
REFERENCE  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
AUTHORS    1 (bases 1 to 742)
            Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE      Full length cDNA of Dictyostelium discoideum at the aggregation
```

```
stage
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source            1..742
     /organism="Dictyostelium discoideum"
     /strain="AX4"
     /db_xref="taxon:44689"
     /clone="dda6b01"
     /clone_lib="Dictyostelium discoideum cDNA library, AF"
     /sex="mat A"
     /dev_stage="Aggregation stage"
BASE COUNT      215 a   142 c   132 g   252 t   1 others
ORIGIN

Query Match      3.0%; Score 58.8; DB 13; Length 742;
Best Local Similarity 44.3%; Pred. No. 1.5e-05;
Matches 295; Conservative 0; Mismatches 362; Indels 9; Gaps 1;

QY 1244 TCAACACCCCGCTGCGTGAATTCAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCT 1303
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 706  TAAATGCACAGTCCGTTCCATATTTCAGATGCCAATCAATGTACCAATTAACACTGATA 647
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1304 CGGCGCGCTGTTCCGAAGCAAAAGGTGGTGTTCGTTACCGACAACATGTTATCCCA 1363
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 646  ACGGTTCAACTTATCGTTCAAAATACATTTGTTGCAATTCACCAACATTTGGCTGGCC 587
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1364 CTTTGACATTTTCACCACTCTTCCGCGGAGAGCAAGCATTTGGCGGAAATCTATCC 1423
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 586  GTATTCAATTATCACCATCTATGCCAAGACGTGATGAACCTCAAAAGAAATGCCAA 527
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1424 TCGGCTACTATAGCAAGATAGTCTTCGTATGGACAACCCGTTGGCGGCAACAAAGCT 1483
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 526  TGGGTTCCGTCATTAACCAATCACCATCTAGGATGAACCATTTCTGGAGAAAAGAGTT 467
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1484 TCTCGGCGCTCCTCCAACTCGAGCTGTGACCCCATCTCAATTTGCCAGAGATACCAATCG 1543
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 466  ATTCAGCTGAAGCCATCTCTGATAAAGTCCAAATCTTTATCTGCTATGACTCTTCAC 407
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1544 AAGTCGATCGGCAATGGTCCATTAACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGT 1603
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 406  ATGACGATGAAGAAACAGCTATCGTTGGTTTCATTCGCTTCAGCCGCTAAAGATTGG 347
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1604 CCCAAGCTCCAAAGAGGTACGACAAAAGTCTCTCTGGGACCAACTCCGCGCAGCCTAGG 1663
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 346  CTGAAAAATCACCAGAGAAAGAGAGAGCCCTCTTAGACTGTTATGCTGTTGGTGG 287
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1664 AGAACCCGGGCGCAAGTCCCGAGCGCGCAACGTCGTCGAAATCGAGTGGTGCAGAGC 1723
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 286  -----GTCCAAAGACATTTATCTCCAAGAAATCTTTTAGAGAAAAGTTGGAAGAAG 236
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1724 AGCAGTATTTCGAAGAGCTCCGAGCGCGCTATGCGCTGAACGATCTCATCACTGG 1783
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 235  AAGAAATATTCAGTGGTGTATTAGTTACACTAGTCCAGGTACTCTCTACCAATGTG 176
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1784 GTTCGCGCTCAGAACCGCGTTCAAGTGTGTTTCATTTGGAACGGAGAGCTCTTTAG 1843
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 175  GTGAACATTTACGTGCTCCAGTTGGTAGAATTCATTTGGGCTGGTACAGAACTGCTTCAG 116
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1844 TTTGGAAGGTTATATGAAGGGCCATAGGATCGGGTCAACGAGGTGCTGCAGAAGTTG 1903
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 115  TTTGGATTGGTTATATGAAGGTGCGCTTAGAATCAGGTTTATAGAGTTTCAAAAGAAATTA 56
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1904 TGGCTA 1909
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 55  AAGATA 50
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 3
BJ373006/c      711 bp      mRNA      linear      EST 08-MAR-2002
LOCUS          BJ373006 Dictyostelium discoideum cDNA library, CF Dictyostelium
DEFINITION     dictyostelium cDNA clone ddc15e09 3', mRNA sequence.
ACCESSION      BJ373006
VERSION        BJ373006.1 GI:19282389
KEYWORDS       EST.
SOURCE          Dictyostelium discoideum.
ORGANISM       Dictyostelium discoideum.
REFERENCE      1 (bases 1 to 711)
AUTHORS        Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE          Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL        Unpublished (2002)
COMMENT        Contact: Tadasu Shin-i
                  Center For Genetic Resource Information
                  National Institute of Genetics
                  1111 Yata, Mishima, Shizuoka 411-8540, Japan
                  Tel: 81-559-81-6856
                  Fax: 81-559-81-6855
                  Email: tshini@genes.nig.ac.jp.
FEATURES       source
                 1..711
                 /organism="Dictyostelium discoideum"
                 /strain="AX4"
                 /db_xref="taxon:44689"
                 /clone="ddc15e09"
                 /clone_lib="Dictyostelium discoideum cDNA library, CF"
                 /sex="mat A"
                 /dev_stage="Culmination stage"
BASE COUNT    219 a 130 c 121 g 240 t      1 others
ORIGIN

Query Match      3.0%; Score 57.8; DB 13; Length 711;
Best Local Similarity 45.1%; Pred. No. 2.8e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

QY 1324 AAAAAGTGGTGGTTTCGTACCGACACATGTTATCCCATCGCTGACATTTTCCACCACT 1383
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 655 AAATACATGTTGTGCAATTCACCAACATTTGGTGGCGGTATTCATTTATTCACCATCT 596

QY 1384 CTTCCCGCGGAGACAGCATTTGGCGAAATCTATCCTCGCTACTATAGCAAGATA 1443
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 ATGCCACCAAGACGTGTGAATCTACTCAAGAATGCCAATGGGTTCGTCATTAAACCC 536

QY 1444 GTCTTCGTATGGGACACCGGTGGCGGAAAGGCTTCTCGGGGGTCTCCCAATCG 1503
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 ATCACCATCTATGATGAACCATTTNCGGAGAAAGAGGTTATTACGTTGAAGCATCTCT 476

QY 1504 AGCTGTGACCCCATCTATTTGCCAGATACCAAGCATCGAAGTCGATCGCAATGGTCC 1563
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 475 GATAAAGGTCCAACTTTTATCTGCTATGATGACTCTTCACATGACGATAAGAAACAGCT 416

QY 1564 ATTACCTGTTTCATGGTCGGACACCGCGGAGTGGTCCACACATCGCAAGCAGGTA 1623
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 415 ATCGTGGTTTCATTTGCTTTACGCCCTAAAGATTGGGTGAAAAATACCCAGAGAA 356

QY 1624 CGACAAAAGTCGTCTGGGACCAACTCCGCGCAGGCTACGAGAACCGCGGGCCCAAGTC 1683
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 AGAAGAGAGCCGCTTAGACTGTTATGCTCGTTGGT-----GGGTCCAAAGCA 305

QY 1684 CCAGAGCCGGCCAGCGTGTGGAATTCGAGTGGTTCGAGACGACAGTATTTTCCAGGAGCT 1743
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 TTATCTCCAAAGAACTTTTATAGAAAAAGTTGGAAGAAGAGAAATATTACGCTGGTTGT 245

QY 1744 CCGAGCCCGCTCTATGGGCTGACACATCTCATCACACTGGGTTCGGCGCTCAGAACCGG 1803
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TATTTAGGTTACACTAGTCCAGGTACTCTACCAATTTGGTGAACATTTACGTGCTCCA 185

QY 1804 TTCAAGTGTGTTCAATTCCTTGGACGGAGAGCTCTTTTAGTTTGGAAAGGTTATAGGAA 1863

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Db 184 GTTGGTAGAATTCATTGGCTGGTGCAGAAACTGCTCAGTTTGGATTGTTATATGGAA 125

QY 1864 GGGGCCATCAGATCGGTTCACAGAGTGTGCAGAGAGTTGTGGCTA 1909
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 GGTGCTTAGAATCAGGTTTGTAGAGTTTCAAAAGAAATTAAGATA 79

RESULT 4
BJ377633/c      730 bp      mRNA      linear      EST 08-MAR-2002
LOCUS          BJ377633 Dictyostelium discoideum cDNA library, CF Dictyostelium
DEFINITION     dictyostelium cDNA clone ddc25101 3', mRNA sequence.
ACCESSION      BJ377633
VERSION        BJ377633.1 GI:19287016
KEYWORDS       EST.
SOURCE          Dictyostelium discoideum.
ORGANISM       Dictyostelium discoideum.
REFERENCE      1 (bases 1 to 730)
AUTHORS        Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE          Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL        Unpublished (2002)
COMMENT        Contact: Tadasu Shin-i
                  Center For Genetic Resource Information
                  National Institute of Genetics
                  1111 Yata, Mishima, Shizuoka 411-8540, Japan
                  Tel: 81-559-81-6856
                  Fax: 81-559-81-6855
                  Email: tshini@genes.nig.ac.jp.
FEATURES       source
                 1..730
                 /organism="Dictyostelium discoideum"
                 /strain="AX4"
                 /db_xref="taxon:44689"
                 /clone="ddc25101"
                 /clone_lib="Dictyostelium discoideum cDNA library, CF"
                 /sex="mat A"
                 /dev_stage="Culmination stage"
BASE COUNT    211 a 141 c 130 g 243 t      5 others
ORIGIN

Query Match      3.0%; Score 57.4; DB 13; Length 730;
Best Local Similarity 44.9%; Pred. No. 3.7e-05;
Matches 263; Conservative 0; Mismatches 314; Indels 9; Gaps 1;

QY 1324 AAAAAGTGGTGGTTTCGTACCGACACATTTGATCCCACTTGACATTTTCCACCATCT 1383
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 611 AAATACATCTGTTGTGCAATTCACCAACATTTGGCTGCGGTATTTCATTATTCACCATCT 552

QY 1384 CTTCCCGCGGAGAGCAAGCATTTGGCGGAAAAATCTATCCTCGGTACTATAGCAAGATA 1443
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 551 ATGCCACCAAGACGTGATGAACCTCACTCAAGAATGCCAATGGGTTCGCGTCATTAAACC 492

QY 1444 GTCTTCGTATGGGACACCGGTGGCGGAAAGGCTTCTCGGGCGTCCCTCAATCG 1503
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 491 ATCACCATCTATGATGAACCATTTCTGGAGAAAAGAGGTTATTTCAGCTGAAGCCATCTCT 432

QY 1504 AGCTGTGACCCCATCTCTCATTTGCGACAGATACCAAGTCGATCGCAATGGTCC 1563
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 431 GATAAAGGTCCTATCTTTATCTGCTATGATGACTCTTCACATGACGATAGAAACAGCT 372

QY 1564 ATTACCTGTTTCATGTCGGAGACCGGGAGCGGAAGTGGTCCCAAGTCCCAAGCAGGTA 1623
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 371 ATCGTTGTTTCATTTGCTGCTTCAGCGCTAAAGATTGGGCTGAAAAATACCCAGAGAA 312

QY 1624 CGACAAAAGTCGTCTGGGACCAACTCCGCGCAGCCTACGAGAACCGCGGGCCCCAAGTC 1683
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 311 AGAAGAGAGACCGCTCTTAGACTGTTATGCTGTTGGT-----GGGTCCAAAGCA 261

QY 1684 CCAGAGCCGGCCACAGCTGCTCGAAATCGAGTGGTTCGAGACGAGTATTTCCAGGAGCT 1743

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Db 260 TTAATCCAAAGAAATCTTTTAGAGAAAAGTTGGAAGAAGAAAGAAATATATTCAGTGGTTGT 201
QY 1744 CCGAGCGCGTCTATGGGTGAACGATCTCATCACACTGGGTTCGCGCTCAGAACGCG 1803
Db 200 TATTTAGGTTACACTAGTCCAGGTACTCTCTACCAATGTGGTGAACATTNACGTCTCCA 141
QY 1804 TTCAAGTGTGTTCAATTCGTTGGACGGAGAGCGTCTTTAGTTTGGAAAGGGTATATGAA 1863
Db 140 GTTGTGAGAAATTCATTTGGGCTGNCAGAAACTGCTTCAGTTTGGATTGGTTATATGAA 81
QY 1864 GGGCCATACGATCGGTCAACGAGTCTGTCGAGAAAGTTGTGGCTA 1909
Db 80 GGTGCTTAGAATCAGGTTTATAGAGTTTCAAAAGAAATTAAGATA 35

RESULT 5
BJ431313/c
LOCUS
DEFINITION
  BJ431313 Dictyostelium discoideum cDNA library, VF Dictyostelium
  discoideum cDNA clone dvl3pl5 3', mRNA sequence.
ACCESSION
  BJ431313
VERSION
  BJ431313.1 GI:19406035
KEYWORDS
  EST.
SOURCE
  Dictyostelium discoideum.
  Dictyostelium discoideum.
ORGANISM
  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
  1 (bases 1 to 610)
  Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
  Full length cDNA of Dictyostelium discoideum at the vegetative
  stage
JOURNAL
  Unpublished (2002)
COMMENT
  Contact: Tadasu Shin-I
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
  Location/Qualifiers
    1..610
      /organism="Dictyostelium discoideum"
      /strain="AX4"
      /db_xref="taxon:44689"
      /clone="dvl3pl5"
      /clone_lib="Dictyostelium discoideum cDNA library, VF"
      /sex="mat A"
      /dev_stage="Growth phase"
      179 a 122 c 107 g 201 t 1 others
BASE COUNT
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ORIGIN

Query Match 3.0%; Score 57.2; DB 13; Length 610;
Best Local Similarity 45.1%; Pred. No. 3.8e-05;
Matches 261; Conservative 0; Mismatches 309; Indels 9; Gaps 1;

QY 1324 AAAAGGTGGTTCGTTACCGACACATGTATCCACCTTGACATTTTCACCACCT 1383
Db 610 AAATACATTTGTTGGCAATTCACCAACATTTGGCTGCTGCTATTCATTTACCATCT 551
QY 1384 CTTCCCGCGAGAACCAAGCATTTGGCGGAAAAATCTATCTCGGTCTACTATAGCAAGATA 1443
Db 550 ATGCCACCAAGACGTGATGACTCACTCAAGATGCCAATGGTTCGCTCATTAAGAAC 491
QY 1444 GTCTTCGTATGGCAACACCGGTGGCGCGAACAAAGCTTCTCGGGCGTCTCCCAATCG 1503
Db 490 ATCACCATCTATGATGAACCATCTGGAGAAAAGAGTTATTTCAGCTGAAGCCATCTCT 431
QY 1504 AGCTGTGACCCCATCTCATTTGCCAGATATACCAGATCGAAGTCGATCGGCATGGTCC 1563
Db 430 GATAAAGTCCCAATCTTATCTGCTATGATGACTCTTCACATGACGATAAGAAAACAGCT 371
QY 1564 ATTACCTGTTTCATCGTCGGAGACCCGGAGAGTGGTCCCAACAGTCCCAACAGGTA 1623
Db 370 ATCGTGTGTTTCATCTGCTGCTTCAGCCGCTAAAGATTGGGCTGAAAATCACCAGAA 311

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QY 1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGACGCTACGAGAACGCCGGGCCAAGTC 1683
Db 310 AGAAGAGAGCCGCTCTTAGACTGTTATGCTCGTTGGT-----GGGTCCAAAGCA 260
QY 1684 CCAGAGCCGGCCAAACGCTCGAATCGAGTGGTGAAGCAGCAGTAGTATTTCCAAAGAGCT 1743
Db 259 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAGAAGAAGAAATATTCACGTGGTTGT 200
QY 1744 CCGAGCCCGCTCTATGGCTGAACGATCTCATCACACTGGTTCGGCGCTCAGAACGCCG 1803
Db 199 TATTTAGGTTACACTAGTCCAGGTACTCTTACCAATGTGTGTAACATTTACGTGCTCCA 140
QY 1804 TTCAAGTGTGTTTCATTTGTTGGAACGGACGCTCTTTAGTTTGGAAAGGGTATATGAA 1863
Db 139 GTTGTAGAATTCAATTGGCGTGGTACAGAACTGCTTCAGTTTGGATTGGTTATATGAA 80
QY 1864 GGGCCCATACGATCGGTGTCACGAGGTGCTGCAGAAAGTT 1902
Db 79 GGTGCTTAGAATCAGGTTTATAGAGTTTCAAAAGAAAT 41

RESULT 6
BJ374786/c
LOCUS
DEFINITION
  BJ374786 Dictyostelium discoideum cDNA library, CF Dictyostelium
  discoideum cDNA clone ddc16d07 3', mRNA sequence.
ACCESSION
  BJ374786
VERSION
  BJ374786.1 GI:19284169
KEYWORDS
  EST.
SOURCE
  Dictyostelium discoideum.
  Dictyostelium discoideum.
ORGANISM
  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
  1 (bases 1 to 611)
  Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
  Full length cDNA of Dictyostelium discoideum at the culmination
  stage
JOURNAL
  Unpublished (2002)
COMMENT
  Contact: Tadasu Shin-I
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
  Location/Qualifiers
    1..611
      /organism="Dictyostelium discoideum"
      /strain="AX4"
      /db_xref="taxon:44689"
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      /sex="mat A"
      /dev_stage="Culmination stage"
      181 a 125 c 113 g 192 t
BASE COUNT
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ORIGIN

Query Match 3.0%; Score 57.2; DB 13; Length 611;
Best Local Similarity 45.1%; Pred. No. 3.8e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

QY 1324 AAAAGGTGGTTCGTTACCGACACATTTGTATCCACCTTGACATTTTCACCACCT 1383
Db 592 AAATACATTTGTTGCAATTCACCAACATTTGGCTGCGGTATTCATTTACCATCT 533
QY 1384 CTTCCCGCGAGAACCAAGCATTTGGCGGAAAAATCTATCTCGGTCTACTATAGCAAGATA 1443
Db 532 ATGCCACCAAGACGTGATGAACCTCACTCAAGAAATGCCAATGGGTTCCGCTCATTAACC 473
QY 1444 GTCTTCGTATGGACAAACCGGTGGCGGACAAAGGCTTCTCGGGCGTCTCCCAATCG 1503
Db 472 ATCACCATCTATGATGAACCATTTCTGGAGAAAAGAGTTATTTCAGCTGAAGCCATCTCT 413

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QY	1504	AGCTGTGACCCCATCTCAATTTGCCAGAGATACCAACATCGGAAGTGCATGCGCATGGTCC	1563
Db	412	GATAAAGGTCCTCAATCTTTATCTGCTATGATGACTCTTCACATGACGATAAAGAAACAGCT	353
QY	1564	ATTACCTGTTTCATGTCGAGACCGCGGACGGAAGTGGTCCCAACAGTCCAAAGCAGTA	1623
Db	352	ATCGTTGGTTTCATGCTGCTTCACCGCTAAAGATTGGCTGAAAAATCACAGAGAA	293
QY	1624	CGAAAAAGTCTGCTGGGACCAACTCCCGCAGAGCTACGAGAACCGCGGGGCCCAAGTC	1683
Db	292	AGAAAGAGAGCGCTCTAGACTGTTATGCTCGTGGT-----GGGGTCCAAAAGCA	242
QY	1684	CCAGAGCGGGCCAACTGCTCGAAATCGAGTGGTGGAGCAGCAGTATTTCCAAAGAGCT	1743
Db	241	TTATCTCCAAAGATCTTTTAGAGAAAAGTTGGAAAGAGAGAAATATTCACGTGGTTGT	182
QY	1744	CCGAGCGCGCTATGGGCTGAACGATCFCATCACACTGGGTTCGGCGCTCAGAACGCGG	1803
Db	181	TATTTAGGTTACACTAGTCCAGTACTCTCTACCAATGGTGGTGAACATTTACGTGCTCCA	122
QY	1804	TTCAAGTGTGTTTCATGTTGGAACGGAGAGCGTCTTTAGTTTGGAAAAGGGTATATGGAA	1863
Db	121	GTGGTAGAATTCATTTGGGCTGTCAGAAAACGCTTCAGTTGGATTGGTTATATGGAA	62
QY	1864	GGGGCCATAGATCGGGTCAACGAGTGTCTGAGAAAGTTGTGGCTA	1909
Db	61	GGTGCCTTAGAATCAGGTTTAGAGTTTCAAAAGAAATTTAAAGATA	16
RESULT 7			
LOCUS	BJ428963/c	612 bp	mRNA linear EST 13-MAR-2002
DEFINITION	BJ428963 Dictyostelium discoideum cDNA library, VF Dictyostelium		
ACCESSION	BJ428963.1	GI:19403685	
VERSION	EST.		
KEYWORDS	Dictyostelium discoideum.		
SOURCE	Dictyostelium discoideum		
ORGANISM	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.		
REFERENCE	1 (bases 1 to 612)		
AUTHORS	Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.		
TITLE	Full length cDNA of Dictyostelium discoideum at the vegetative stage		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.		
FEATURES	source		
	1. .612		
	/organism="Dictyostelium discoideum"		
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	/sex="mat A"		
	/dev_stage="growth phase"		
BASE COUNT	180 a	125 c	113 g 194 t
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Query Match	3.08;	Score 57.2;	DB 13; Length 612;
Best Local Similarity	45.1%;	Pred. No. 3.8e-05;	
Matches	264;	Conservative 0;	Mismatches 313; Indels 9; Gaps 1;
QY	1324	AAAAAGGTGGTGGTTCGTTACCGACACATCTGTATCCCACTTGACATTTTCACCACT	1383
Db	591	AAATACATGTTGTTGCAATTCACCAACATCGGTGGCGGTATTCATTTACCACT	532
QY	1384	CTTCCCGCCGAGAACGATTTGGCGGAAAAATCTATCTCCGCTACTATAGCAAGATA	1443

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QY 1324 AAAAGGTGGTGGTTCGTACCGACAAACATGTATCCACCTTGACATTTTCACCACT 1383
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Db 617 AAATACATTTGTTGCAATCCACCAACATGGCTGGCGGTATTCATATTCACCACT 558
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QY 1384 CTTCCCGCGGAGAAGCAGCATGGCGGAAAATCTATCCTCGGCTACTATAGCAAGATA 1443
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QY 1444 GTCTTCGTATGGACAAACCGGTGGCGGACAAAGCCTTCCTGGGCGTCTCAATCG 1503
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Db 497 ATCACATCTATGATGAACCATCTTGAGAGAAAGAGGTATTCAGCTGAAGGCCATCTCT 438
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QY 1504 AGCTGTGACCCCATCTATTTGCCAGAGATACCAATCGATCGATCGGCAATGGTCC 1563
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Db 437 GATAAAGGTCCAACTTTATCTGCTATGATGACTCTTCACATGAGGATAAGAAACAGCT 378
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QY 1564 ATTACCTGTTTCATGGTCGGAGACCGGGAGGAGTGGTCCCAACAGTCCCAAGAGTA 1623
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Db 377 ATCGTGGTTCATTTGCTGCTTTCAGCCCTAAAGATTGGGCTGAAAAATCACCAGAAGAA 318
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QY 1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTACGAGAGCGCGGCCCAAGTC 1683
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Db 317 AGAAGAGAGCGCTTTAGACTGTTATGCTGTTGCT-----GGGTCCAAAAGCA 267
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QY 1684 CCAGAGCGGCGCAACGCTCGAATCGAGTGGTGGAGCAGCAGTATTTCCAAAGAGCT 1743
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Db 266 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAGAAAGAAATATTCACGTTGTTGT 207
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QY 1744 CCGAGCGCGTCTATGCGCTGAACGATCTCATCAGCTGGGTTCCGCGCTCAGAACGCG 1803
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Db 206 TATTTAGGTTACAGTAGTCCAGGTACTCTACCAATGGTGAACATTTACGTGCTCCA 147
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QY 1804 TTCAAGTGTGTTCAATTCGTTGGAACGAGAGCTCTTTAGTTTGGAAAGGTATATGAA 1863
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Db 146 GTTGCTAGAAATTCATTTGGCTGGTACAGAACTGCTTCAGTTTGGATTGTTATATGAA 87
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QY 1864 GGGGCCATACAGTCGGGTCAACGAGTGCTGCAGAAGTTGGGCTA 1909
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Db 86 GGTGCTTAGAATCAGGTTTATAGAGTTTCAAAGAAAATTAAGATA 41
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RESULT 9
LOCUS BJ375424 648 bp mRNA linear EST 08-MAR-2002
DEFINITION BJ375424 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc18m13 3', mRNA sequence.
ACCESSION BJ375424
VERSION BJ375424.1 GI:19284807
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 648) Dictyostellida; Dictyostelium.
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 648
/organism="Dictyostelium discoideum"
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/sex="mat A"

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Best Local Similarity 45.1%; Pred. No. 3.9e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;
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Db 626 AAATACATTTGTTGCAATTCACCAACATTTGGCTGGCGGTATTCATATTCACCACT 567
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QY 1384 CTTCCCGCGGAGAAGCAGCATGGCGGAAAATCTATCCTCGGCTACTATAGCAAGATA 1443
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Db 506 ATCACATCTATGATGAACCATTTCTGAGAAAAGAGTTATTCAGCTGAAGCCATCTCT 447
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QY 1504 AGCTGTGACCCCATCTATTTGCCAGAGATACCAATCGATCGAAGTCATCGGCAATGGTCC 1563
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Db 446 GATAAAGGTCCAACTTTATCTGCTATGATGACTCTTCACATGAGGATAAGAAACAGCT 387
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QY 1564 ATTACCTGTTTCATGGTCGGAGACCGCGGACGGAAGTGGTCCCAACAGTCCCAAGAGTA 1623
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Db 386 ATCGTGGTTCATTTGCTGCTTCAGCGCTAAAGATTGGCTGAAAAATCACCAGAAGAA 327
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QY 1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTACGAGAACCGCGGCCCAAGTC 1683
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Db 326 AGAAGAGAGCGCTCTTAGACTGTTATGCTGCTGTTGCT-----GGGTCCAAAAGCA 276
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QY 1684 CCAGAGCGGCGCAACGCTCGAATCGAGTGGTCCCAACAGCAGCAGTATTTCCAAAGAGCT 1743
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Db 275 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAGAAAAGAAATATTCACGTTGTTGT 216
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QY 1744 CCGAGCGCGCTCTATGGGCTGAACGATCTCATCAGCTGGGTTCCGCGCTCAGAACGCG 1803
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Db 215 TATTTAGGTTACACTAGTCCAGTACTCTCTACCAATGGTGAACATTTAGCTGCTCCA 156
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QY 1804 TTCAAGTGTGTTCAATTCGTTGGAACGAGAGCTCTTTAGTTTGGAAAGGTATATGAA 1863
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QY 1864 GGGGCCATACGATCGGCTCAACGAGGTGCTGCAGAAGTTGTGCTA 1909
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RESULT 10
LOCUS BJ375565/c 650 bp mRNA linear EST 08-MAR-2002
DEFINITION BJ375565 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc19m05 3', mRNA sequence.
ACCESSION BJ375565
VERSION BJ375565.1 GI:19284948
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 650) Dictyostellida; Dictyostelium.
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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FEATURES

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source 1..650
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc19m05"
/clonelib="Dictyostelium discoideum cDNA library, Cf"
/sex="mat A"
/dev_stage="Culmination stage"

BASE COUNT 192 a 124 c 113 g 221 t
ORIGIN

Query Match 3.0%; Score 57.2; DB 13; Length 650;
Best Local Similarity 45.1%; Pred. No. 3.9e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

QY 1324 AAAAAGTGGTGGTTTCGTACCGACAAATGTATCCCACTTGACATTTTCACCACT 1383
Db 633 AAATACATTTGTTGCAATTCACCAACATTTGGCTGGCGGTATTCATTTATCACCATCT 574

QY 1384 CTTCGCCGAGAACAGCATTTGGCGGAAAAATCTATCCTCGCTACTATAGCAAGATA 1443
Db 573 ATGCCACAGACGTGATGAATCCTCAAGAAATGCCAATGGTTCCGTTCATTAAGACC 514

QY 1444 GTCTTCGTATGGGACACCCGTGTGGCGGACAAAGCTTCTCGGCGCTCCTCCAATCG 1503
Db 513 ATCACCATCTATGATGAACCATTTCTGGAGAAAAGAGGTTATTTCAGCTGAAGCCATCTCT 454

QY 1504 AGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGATCGAAGTCGATCGCAATGGTCC 1563
Db 453 GATAAAGGTCCAAATCTTATCTGTATGATGACTCTTCACATGACGATAGAAAACAGCT 394

QY 1564 ATTACCTGTTTCATGTCGGAGACCCGGAGGAGTGGTCCCAACAGTCCCAAGCAGGTA 1623
Db 393 ATCGTTGTTTCATGCTGCTTCAGCCGCTTAAGATTTGGCTGAAATATCACCAGAGAA 334

QY 1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCCTACGAGAACGCCGGGCCCAAGTC 1683
Db 333 AGAAGAGAGCGCTTAGACTGTTATGCTGCTTGGT-----GGGGTCCAAAAGCA 283

QY 1684 CCAGAGCCGGCCACGTCCTGAATCGAGTGGTCGAGCAGCAGTATTTCCAAAGGAGCT 1743
Db 282 TTATCTCCAAGAATCTTTTATAGAAAAGTTTGAAGAAAGAAAGATATTCACGTGGTGT 223

QY 1744 CCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCCGCGCTCAGAACGCCG 1803
Db 222 TATTAGTTTACACTAGTCCAGGTACTCTTACCATGTGTTGACATTTACGTGCTCCA 163

QY 1804 TTCAAGTGTGTTTCATTTGTTGGAACGAGACGTCCTTTAGTTTGGAAAGGATATATGAA 1863
Db 162 GTTGGTAGAATTCATTTGGGCTGGTACAGAACTGCTTCAGTTTGGATTGGTTATATGAA 103

QY 1864 GGGGCCATACGATCGGTCACAGAGTGTCTGCAGAAAGTTGTGGCTA 1909
Db 102 GGTGCCTTAGAATCAGGTTTATAGAGTTTCAAAAAGAAATTAAGATA 57

RESULT 11
BJ372067/c 651 bp mRNA linear EST 08-MAR-2002
LOCUS BJ372067 Dictyostelium discoideum cDNA library, Cf Dictyostelium
DEFINITION dictyostelium cDNA clone ddc1k04 3', mRNA sequence.
ACCESSION BJ372067
VERSION BJ372067.1 GI:19281450
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
REFERENCE 1 (bases 1 to 651)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
TITLE Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
```

```
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
Location/Qualifiers
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/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc1k04"
/clonelib="Dictyostelium discoideum cDNA library, Cf"
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/dev_stage="Culmination stage"

BASE COUNT 191 a 124 c 113 g 223 t
ORIGIN

Query Match 3.0%; Score 57.2; DB 13; Length 651;
Best Local Similarity 45.1%; Pred. No. 3.9e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

QY 1324 AAAAAGTGGTGGTTTCGTACCGACAAATGTATCCCACTTGACATTTTCACCACT 1383
Db 634 AAATACATTTGTTGCAATTCACCAACATTTGGCTGGCGGTATTCATTTATCACCATCT 575

QY 1384 CTTCGCCGAGAACAGCATTTGGCGGAAAAATCTATCCTCGCTACTATAGCAAGATA 1443
Db 574 ATGCCACAGAGCTGATGAATCCTCAAGAAATGCCAATGGTTCCGTTCATTAAGACC 515

QY 1444 GTCTTCGTATGGGACAAACCCGTGTGGCGGACAAAGCTTCTCGGCGCTCCTCCAATCG 1503
Db 514 ATCACCATCTATGATGAACCATTTCTGGAGAAAAGAGGTTATTTCAGCTGAAGCCATCTCT 455

QY 1504 AGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGATCGAAGTCGATCGCAATGGTCC 1563
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Db 394 ATCGTTGTTTCATGCTGCTTCAGCCGCTTAAGATTTGGCTGAAATATCACCAGAGAA 335

QY 1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCCTACGAGAACGCCGGGCCCAAGTC 1683
Db 334 AGAAGAGAGCGCTCTAGACTGTTATGCTGCTTGGT-----GGGGTCCAAAAGCA 284

QY 1684 CCAGAGCCGGCCACGTCCTGAATCGAGTGGTCGAAACGACGATTTTCCAAAGGAGCT 1743
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DEFINITION dictyostelium cDNA clone ddv9b03 3', mRNA sequence.
ACCESSION BJ430839
VERSION BJ430839.1 GI:19405561
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
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Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
1 (bases 1 to 658)  
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.  
Full length cDNA of Dictyostelium discoideum at the vegetative  
stage  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshiniegenes.nig.ac.jp.  
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DEFINITION BJ429162 Dictyostelium discoideum cDNA clone ddv2f15 3', mRNA sequence.
ACCESSION BJ429162.1 GI:19403884
VERSION BJ429162.1
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 687)
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
TITLES Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the vegetative
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
LOCATION/Qualifiers
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Qy 1304 CGGCGCGCTGTCGGAAGCAAAAGGTGGTGTTCGTTACCGACACACATTGTATCCCA 1363
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DEFINITION BJ375168 Dictyostelium discoideum cDNA clone ddcl7n18 3', mRNA sequence.
ACCESSION BJ375168
VERSION BJ375168.1 GI:19284551
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 694)
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
TITLES Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
LOCATION/Qualifiers
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Best Local Similarity 45.1%; Pred. No. 4.1e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 153338381 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1851.4	96.0	1930	4	US-09-352-159-39 Sequence 39, Appl
4	1792.2	92.9	1928	4	US-09-352-159-43 Sequence 43, Appl
5	1789	92.7	1928	4	US-09-352-159-45 Sequence 45, Appl
6	1787.4	92.7	1928	4	US-09-352-159-41 Sequence 41, Appl
7	1602.6	83.1	1803	4	US-09-352-159-22 Sequence 22, Appl
8	1602.6	83.1	1803	4	US-09-352-168-22 Sequence 22, Appl
9	1596.2	82.7	2490	4	US-09-352-159-32 Sequence 32, Appl
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14	1212.2	62.8	2976	4	US-09-352-168-26 Sequence 26, Appl
15	1212.2	62.8	3003	4	US-09-352-159-24 Sequence 24, Appl
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17	1212.2	62.8	3591	4	US-09-352-159-30 Sequence 30, Appl
18	1212.2	62.8	3591	4	US-09-352-168-30 Sequence 30, Appl
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c 45	33.2	1.7	2743	4	US-09-060-482-3	Sequence 3, Appl

ALIGNMENTS

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; Patent No. 6211434  
; GENERAL INFORMATION:  
; APPLICANT: Duvick, Jonathan P.  
; APPLICANT: Gilliam, Jacob T.  
; APPLICANT: Maddox, Joyce R.  
; TITLE OF INVENTION: Amino Polyol Amine Oxidase  
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use  
; FILE REFERENCE: 1134  
; CURRENT APPLICATION NUMBER: US/09/352,159A  
; CURRENT FILING DATE: 1999-07-12  
; EARLIER APPLICATION NUMBER: 60/092,936  
; EARLIER FILING DATE: 1998-07-25  
; EARLIER APPLICATION NUMBER: 60/135,391  
; EARLIER FILING DATE: 1999-05-21  
; NUMBER OF SEQ ID NOS: 46  
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; NAME/KEY: Intron  
; LOCATION: (739)...(811)  
; NAME/KEY: Intron  
; LOCATION: (1134)...(1186)  
US-09-352-159-35

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Db	901	GAGCCCTCAGGGCAAGGGGCTCGACAGTGTGAGCTTCGCGCACACTGTGAGAAGACCT	960
Qy	961	AACTTGCCTGTCTTCTCAGCGTGCAAAACAGATCACCGCGTCTGTCTGGTGTGGGA	1020
Db	961	AACTTGCCTGTCTTCTCAGCGTGCAAAACAGATCACCGCGTCTGTCTGGTGTGGGA	1020
Qy	1021	AGCCACAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGGCCACGGGTCTCAG	1080
Db	1021	AGCCACAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGGCCACGGGTCTCAG	1080
Qy	1081	TAATATTGTCTCGGACAAGAAAGCGGGGGCAGTATATCGGATGCAAAACAGGTGGGTG	1140
Db	1081	TAATATTGTCTCGGACAAGAAAGCGGGGGCAGTATATCGGATGCAAAACAGGTGGGTG	1140
Qy	1141	CGGTGCTCTCAGGTAGGGGACTCGTTTCTTAGTGTGTCATTCCAGGTATGCACTCGATT	1200
Db	1141	CGGTGCTCTCAGGTAGGGGACTCGTTTCTTAGTGTGTCATTCCAGGTATGCACTCGATT	1200
Qy	1201	TGCCATGCCATGTCAAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT	1260
Db	1201	TGCCATGCCATGTCAAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT	1260
Qy	1261	GGAAATTGACAGTCTGGGCTCGGCTGTATGTATACGATCGGCTCGGGGGCGGTGTCCGA	1320
Db	1261	GGAAATTGACAGTCTGGGCTCGGCTGTATGTATACGATCGGCTCGGGGGCGGTGTCCGA	1320
Qy	1321	AGCAAAAAGGTGCTGGTTCGTTTACCAGCAACATTTGATCCCACTTGCACATTTTTCACCA	1380

Db	1321	AGCAAAAGTGTGTGTTTCGTTTACGCAACATGTATCCCACTTCACATTTTCACCA	1380
Qy	1381	CCCTCTTCCCGCCGAGAAGCAAGCAATTTGGCGGAAAAATCTATCTTCGGCTACTATAGCAAG	1440
Db	1381	CTCTCTTCCCGCCGAGAAGCAAGCAATTTGGCGGAAAAATCTATCTTCGGCTACTATAGCAAG	1440
Qy	1441	ATAGTCTTCTGTATGGAGAACACCGTGGTGGCGCGGAACAAAGGTTCTCGGGCGTCTCTCAA	1500
Db	1441	ATAGTCTTCTGTATGGAGAACACCGTGGTGGCGCGGAACAAAGGTTCTCGGGCGTCTCTCAA	1500
Qy	1501	TCGAGCTGTGACCCCATCTCAATTTGCCAGAGATACCAAGCATCGAAGTCGATCGGCAATGG	1560
Db	1501	TCGAGCTGTGACCCCATCTCAATTTGCCAGAGATACCAAGCATCGAAGTCGATCGGCAATGG	1560
Qy	1561	TCCATTTACTTGTTTCATGTGTCGGAGACCCGGGACGGGAAGTGGTCCCAACAGTCCCAAGCAG	1620
Db	1561	TCCATTTACTTGTTTCATGTGTCGGAGACCCGGGACGGGAAGTGGTCCCAACAGTCCCAAGCAG	1620
Qy	1621	GTACGACAAAAGTCTGCTGTGGACCAACATTCGCGCGAGCCTACGAGAAGCCGCGGCGCCAA	1680
Db	1621	GTACGACAAAAGTCTGCTGTGGACCAACATTCGCGCGAGCCTACGAGAAGCCGCGGCGCCAA	1680
Qy	1681	GTCCGAGAGCGGCCAACAGTCTCGAAATCGAGTGGTGAAGCAGCAGTATTTCCAAGGA	1740
Db	1681	GTCCGAGAGCGGCCAACAGTCTCGAAATCGAGTGGTGAAGCAGCAGTATTTCCAAGGA	1740
Qy	1741	GTCGCGAGCGCGTCTATGGGCTGAACGATCTCATCACATGGGTCGCGCCTCAGAAGC	1800
Db	1741	GTCGCGAGCGCGTCTATGGGCTGAACGATCTCATCACATGGGTCGCGCCTCAGAAGC	1800
Qy	1801	CCGTTCAAGTGTCTCATTTTCGTTGGACGAGAGCGTCTTTAGTTTGAAAGGTTATATG	1860
Db	1801	CCGTTCAAGTGTCTCATTTTCGTTGGACGAGAGCGTCTTTAGTTTGAAAGGTTATATG	1860
Qy	1861	GAAGGGCCATACGATCGGGTCAACGAGTGTCTGAGAAATTTGGCTAGCCTGGTGCCA	1920
Db	1861	GAAGGGCCATACGATCGGGTCAACGAGTGTCTGAGAAATTTGGCTAGCCTGGTGCCA	1920
Qy	1921	GCAGCATAG 1929	
Db	1921	GCAGCATAG 1929	
RESULT 2			
US-09-352-159-37			
; Sequence 37, Application US/09352159A			
; Patent No. 6211434			
; GENERAL INFORMATION:			
; APPLICANT: Duwick, Jonathan P.			
; APPLICANT: Gilliam, Jacob T.			
; APPLICANT: Maddox, Joyce R.			
; TITLE OF INVENTION: Amino Polyol Amine Oxidase			
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods			
; FILE REFERENCE: 1134			
; CURRENT APPLICATION NUMBER: US/09/352,159A			
; CURRENT FILING DATE: 1999-07-12			
; EARLIER APPLICATION NUMBER: 60/092,936			
; EARLIER FILING DATE: 1998-07-25			
; EARLIER APPLICATION NUMBER: 60/135,391			
; EARLIER FILING DATE: 1999-05-21			
; NUMBER OF SEQ ID NOS: 46			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 37			
; LENGTH: 1929			
; TYPE: DNA			
; ORGANISM: Exophiala spinifera			
; FEATURE:			
; NAME/KEY: intron			
; LOCATION: (739)...(811)			
; NAME/KEY: intron			
; LOCATION: (1134)...(1186)			
US-09-352-159-37			

Query Match				99.8%; Score 1925.8; DB 4; Length 1929;			
Best Local Similarity				99.9%; Pred. No. 0;			
Matches 1927; Conservative				0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	ATGGCACTTGCACCGAGCTACATCAATCCCAACAGCTCGCCTCCCGACGAGGTATTCC	60				
Db	1	ATGGCACTTGCACCGAGCTACATCAATCCCAACAGCTCGCCTCCCGACGAGGTATTCC	60				
QY	61	CACATCGGGGTAGGGCCCAACAAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA	120				
Db	61	CACATCGGGGTAGGGCCCAACAAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA	120				
QY	121	GAGCTTTGGGCGTGACAGACCCAGCCCTACGAGAAACAGGTTGCCCAAGCAATTGCGCAAT	180				
Db	121	GAGCTTTGGGCGTGACAGACCCAGCCCTACGAGAAACAGGTTGCCCAAGCAATTGCGCAAT	180				
QY	181	CTGGAGCTTGGCTTGTGTCAGTTGGAGCCTCTTCAAAAGCAGCTACCAAGCTCAATTAC	240				
Db	181	CTGGAGCTTGGCTTGTGTCAGTTGGAGCCTCTTCAAAAGCAGCTACCAAGCTCAATTAC	240				
QY	241	TACATCGTGCAGTACGCCGCCGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC	300				
Db	241	TACATCGTGCAGTACGCCGCCGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC	300				
QY	301	TTTGCCCTTGACAGGTCCTCCTTTCACGCTGTGTGCCAGTACCGGCCCTTGGCTTCACCT	360				
Db	301	TTTGCCCTTGACAGGTCCTCCTTTCACGCTGTGTGCCAGTACCGGCCCTTGGCTTCACCT	360				
QY	361	GAATACCTCTTTGAGGTTGATGCCACGGCGCTGTGTGCCAGACACTCACGCCGAGCAAC	420				
Db	361	GAATACCTCTTTGAGGTTGATGCCACGGCGCTGTGTGCCAGACACTCACGCCGAGCAAC	420				
QY	421	GTTCGGGAGCTGTAGTGTGGGCGCTGGCTTTGAGCGTGTGGAGACGGCACGCAAAAGTC	480				
Db	421	GTTCGGGAGCTGTAGTGTGGGCGCTGGCTTTGAGCGTGTGGAGACGGCACGCAAAAGTC	480				
QY	481	CAGGCGCGCGGTCTGTCTGCTGCTCTTGTGAGCGCATGGATCGTGTAGGGGAAAGACT	540				
Db	481	CAGGCGCGCGGTCTGTCTGCTGCTCTTGTGAGCGCATGGATCGTGTAGGGGAAAGACT	540				
QY	541	CTGAGCGTACATCCGGTCCGGCAGGAGGACTATCAACAGCCTCGGCGCTGCGTGGATC	600				
Db	-541	CTGAGCGTACATCCGGTCCGGCAGGAGGACTATCAACAGCCTCGGCGCTGCGTGGATC	600				
QY	601	AATGACAGCAACAAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGGCGAG	660				
Db	601	AATGACAGCAACAAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGGCGAG	660				
QY	661	CTCCAGAGACGACCGGAAATTCATTCATCAAGCACAAAGCGGTACAAACCACCTACAGCT	720				
Db	661	CTCCAGAGACGACCGGAAATTCATTCATCAAGCACAAAGCGGTACAAACCACCTACAGCT	720				
QY	721	CCTTATGTTGACTCCCGGTAGACAAATCCCACTTTGTGATGAGACCTCTGTGAGTGT	780				
Db	721	CCTTATGTTGACTCCCGGTAGACAAATCCCACTTTGTGATGAGACCTCTGTGAGTGT	780				
QY	781	AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGTTGCAAGTGCACCTTGC	840				
Db	781	AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGTTGCAAGTGCACCTTGC	840				
QY	841	GGAATCTCTCCCGTATGGTCTCAGTGCAGAGTATAGCCCTTGAAGACCCCAAGGC	900				
Db	841	GGAATCTCTCCCGTATGGTCTCAGTGCAGAGTATAGCCCTTGAAGACCCCAAGGC	900				
QY	901	GAGCCCTCAGGCGAAGCGGCTGCAGATGTGAGCTTCCGCACTACTGTGAGAAGGACCT	960				
Db	901	GAGCCCTCAGGCGAAGCGGCTGCAGATGTGAGCTTCCGCACTACTGTGAGAAGGACCT	960				
QY	961	AAACTTGCTGCTGTCTCAGGTTGGCAAAACAGATACACGCGCTCTGCTGGTGTGGA	1020				
Db	961	AAACTTGCTGCTGTCTCAGGTTGGCAAAACAGATACACGCGCTCTGCTGGTGTGGA	1020				

RESULT 3  
US-09-352-159-39  
; Sequence 39, Application US/09352159A  
; Patent No. 6211434  
; GENERAL INFORMATION:  
; APPLICANT: Duviok, Jonathan P.  
; APPLICANT: Gilliam, Jacob T.  
; APPLICANT: Maddox, Joyce R.

QY	1021	AGCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGCCCAACCGGTCTCAG	1080
Db	1021	AGCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGCCCAACCGGTCTCAG	1080
QY	1081	TAATATTGTCGCGACAAGAAAGACGGCGGCAGTATATCGATGCAAAACAGGTGCGTG	1140
Db	1081	TAATATTGTCGCGACAAGAAAGACGGCGGCAGTATATCGATGCAAAACAGGTGCGTG	1140
QY	1141	CGGTGCTCTCTCAGGTAGGGAAGTCTGTTCTTAGTGGTCAATCCAGGTATGCAAGT	1200
Db	1141	CGGTGCTCTCTCAGGTAGGGAAGTCTGTTCTTAGTGGTCAATCCAGGTATGCAAGT	1200
QY	1201	TGCCATGCCATGTCAAAAGGAACCTTGTTCCAGGCTCAGTGACACCTCAACACCCCGCTCGCT	1260
Db	1201	TGCCATGCCATGTCAAAAGGAACCTTGTTCCAGGCTCAGTGACACCTCAACACCCCGCTCGCT	1260
QY	1261	GGAAATTGAGCAGTCGGGCTCCGGCTGTATAGTACGATCGGCCTCGGGCGCGTTC	1320
Db	1261	GGAAATTGAGCAGTCGGGCTCCGGCTGTATAGTACGATCGGCCTCGGGCGCGTTC	1320
QY	1321	AGCAAAAAGTGTGTGTTTACCGACAACATTTGATCCCACTTGACATTTTCACCA	1380
Db	1321	AGCAAAAAGTGTGTGTTTACCGACAACATTTGATCCCACTTGACATTTTCACCA	1380
QY	1381	CCTCTTCCCGCGAGAAAGCAATTTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG	1440
Db	1381	CCTCTTCCCGCGAGAAAGCAATTTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG	1440
QY	1441	ATAGTCTTGTATGGGACAACCGTGTGTGGCGGCAACAGGCTTCTCGGGCGTCTCCAA	1500
Db	1441	ATAGTCTTGTATGGGACAACCGTGTGTGGCGGCAACAGGCTTCTCGGGCGTCTCCAA	1500
QY	1501	TCGAGCTGTGACCCCTCATTTGCCAGAGATACCAGCATCGAAGTCCGATCGGCAATGG	1560
Db	1501	TCGAGCTGTGACCCCTCATTTGCCAGAGATACCAGCATCGAAGTCCGATCGGCAATGG	1560
QY	1561	TCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAAGTGGTCCCAACAGTCCAAAGCAG	1620
Db	1561	TCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAAGTGGTCCCAACAGTCCAAAGCAG	1620
QY	1621	GTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTACGAGAACGCCGGGCCCAA	1680
Db	1621	GTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTACGAGAACGCCGGGCCCAA	1680
QY	1681	GTCCACAGCGCGGCAACAGTCTCGAAATCGAGTGTGCGAAGCAGCAGTATTTCCAAAGGA	1740
Db	1681	GTCCACAGCGCGGCAACAGTCTCGAAATCGAGTGTGCGAAGCAGCAGTATTTCCAAAGGA	1740
QY	1741	GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACTGGGTTCCGGCTCAGAAGC	1800
Db	1741	GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACTGGGTTCCGGCTCAGAAGC	1800
QY	1801	CGGTTCAAGTGTGTTCAATTTGCGTTGGAAACGAGACGCTTTTACTTTGGAAGGTTATG	1860
Db	1801	CGGTTCAAGTGTGTTCAATTTGCGTTGGAAACGAGACGCTTTTACTTTGGAAGGTTATG	1860
QY	1861	GAGGGGCCATACGATCGGCTCAACGAGGTCGCGAAGTTCGTGCTAGCCTGGTGGCA	1920
Db	1861	GAGGGGCCATACGATCGGCTCAACGAGGTCGCGAAGTTCGTGCTAGCCTGGTGGCA	1920
QY	1921	GCAGCATAG 1929	
Db	1921	GCAGCATAG 1929	

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; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (739)...(811)
; NAME/KEY: Intron
; LOCATION: (1134)...(1187)
; NAME/KEY: misc.feature
; LOCATION: (648)...(648)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-159-39
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Query Match          96.0%; Score 1851.4; DB 4; Length 1930;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 1 ATGGCACTTGGACCGAGCTACATCAATCCCCAAACGTCGCGCTCCCGAGCAGGCTATTCC 60
Db 1 ATGGCACTTGGACCGAGCTACATCAATCCCCAAACGTCGCGCTCCCGAGCAGGCTATTCT 60

QY 61 CACATCGGCGTAGGCCCAACCAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120
Db 61 CACGTGCGGCTAGGCCAGCGAGGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120

QY 121 GACGCTTTGGGGGCTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180
Db 121 GACGCTTTGGGGGCTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180

QY 181 CTGCGAGCTTGGCTTGTGTCAGTTGGAGCCACTTCAAAACGAGCTCACCAGCTCAATTTAC 240
Db 181 CTGCGAGCTTGGCTTGTGTCAGTTGGAGCCACTTCAAAACGAGCTCACCAGCTCAATTTAC 240

QY 241 TACATCGTCGACTACGCCCGGAGCAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC 300
Db 241 TACATCGTCGACTACGCCCGGAGCAACTCACCGCAATTGGAGATGGGCTGAAGGCTACC 300

QY 301 TTGCGCCTTGACAGGCTCCCTCTTGCAGGCTGGTGCCAGTACCGGCGCTTGGCTTCACT 360
Db 301 TTGCGCCTTGACAGGCTCCCTCTTGCAGGCTGGTGCCAGTACCGGCGCTTGTCTTCACT 360

QY 361 GAATACCTCTTGGAGTTGATCCACGGCGTGGTGCCAGGACACTCGACCCAGACAAAC 420
Db 361 GAATACCTCTTGGAGTTGATCCACGGCGTGGTGCCGGGACACACGACCCAGACAAAC 420

QY 421 GTTGGCGAGCTGGTATGTTGGGCGCTGGCTTGAGCGTTGAGACGCGACGCAAAAGTC 480
Db 421 GTTGGCGAGCTGGTATGTTGGGCGCTGGCTTGAGCGTTGAGACGCGACGCAAAAGTC 480

QY 481 CAGGCGCGCGGCTGTCTCTCGCTTCTTGGAGCGATGGATCGTGTAGGGGGAAGACT 540
Db 481 CAGGCGCGCGGCTGTCTCTCGCTTCTTGGAGCGATGGATCGTGTAGGGGGAAGACT 540

QY 541 CTGAGCGTACAATCGGGTCCCGGAGGAGGACTATCAACGACCTCGGCGCTGGCTGGATC 600
Db 541 CTGAGCGTACAATCGGGTCCCGGAGGAGGACTATCAACGACCTCGGCGCTGGCTGGATC 600

QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCAATTTGAGGGCCAG 660
Db 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCAATTTGAGGGCCAG 660
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QY 661 CTCAGAGACGACCGGAAATTCATCCATCAAGCACAAAGACGGTACAAACCACTACAGCT 720
Db 661 CTCAGAGACGACCTGGAATTCATCCATCAAGCACAAAGACGGTACAAACCACTACAGCT 720

QY 721 CCTTATGGTGACTCCCGGGTAAGACAATCCCACTTTGTGATGAGACCTCTGTGCGAGTGT 780
Db 721 CCTTATGGTGACTCCCTTGGTAAGACAATCCCACTTTGTGATGAGACCTCTGTGCGAGTGT 780

QY 781 AGAATACAGTCACTGACTCCACCTCGTCCAGCTGAGCGAGGAGTTGCAAGTGCACCTTGC 840
Db 781 AGAATACAGTCACTGATTCACCTCGTCCAGCTGAGCGAGGAGTTGCAAGTGCACCTTGC 840

QY 841 GGAATCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCTTTCAAGACCCCAAGGC 900
Db 841 GGAATCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCTTTCAAGACCTCAAGGC 900

QY 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGGCGCACTACTGTGAGAAGACCT 960
Db 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGGCGCACTACTGTGAGAAGAACT 960

QY 961 AAATCTGCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGGA 1020
Db 961 AAATCTGCTGCTGTTCTCGCGGTAGCAAAACAGATCACACGCGCTCTGCTCGGTGTGGA 1020

QY 1021 AGCCACGAGATCAGCATGCTTTTCTCACCGCACTACATCAAGAGTGCCACCGGCTCTCAG 1080
Db 1021 AGCCACGAGATCAGCATGCTTTTCTCACCGCACTACATCAAGAGTGCCACCGGCTCTCAG 1080

QY 1081 TAATATTGCTCGGACAAGAAAGACGGCGGAGTATATGCGATGCAAAACAGAGTGCCTG 1140
Db 1081 TAATATTGCTCGGACAAGAAAGACGGCGGAGTATATGCGATGCAAAACAGAGTGCCTG 1140

QY 1141 CGGTGCTCTCTCAGTAGGGACTCGTCTTCT-TAGTGGTCAATTCAGGATGACAGTTCGAT 1199
Db 1141 TGGTGTGCTCTCAGTGGGAGTCTGTTCTCAAGTGGTCAATTCAGGATGACAGTTCGAT 1200

QY 1200 TTGCGATGCCATGTCAAAGAACTTTGTCAGGCTCAGTGCACCTCAACACCCCGCTCGC 1259
Db 1201 TTGCGATGCCATGTCAAAGAACTTTGTCAGGCTCAGTGCACCTCAACACCCCGCTCGC 1260

QY 1260 TGGAAATTGAGCAGTCCGGCTCCGGCTGTATAGTACGATCGGCTCTCGGGCGCTGTCCG 1319
Db 1261 TGAATTTGAGCAGTCCGGCTCCGGCTGTACAGTACGATCGGCTCTCGGGCGCTGTCCG 1320

QY 1320 AAGCAAAAGGTGGTGGTTTTCGTACCGACAATTTGTATCCCACTTGACATTTTCACC 1379
Db 1321 AAGCAAAAGGTGGTGGTTTTCGTACCGACAATTTGTATCCCACTTGACATTTTCACC 1380

QY 1380 ACCTCTTCCCGCGGAGAAAGCAAGCATTTGGCGAAAATCTATCCTCGGCTACTATAGCAA 1439
Db 1381 ACCTCTTCCCGCGGAGAAAGCAAGCATTTGGCGAAAATTTCTATCCTGGGCTACTATAGCAA 1440

QY 1440 GATAGTCTTGTATGGGACAACCGGTGGCGGCAACAGGCTTCTCGGGCGCTCTCTCCA 1499
Db 1441 GATAGTCTTGTATGGGACAACCGGTGGCGGCAACAGGCTTCTCGGGCGCTCTCTCCA 1500

QY 1500 ATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCGATCGAAGTCGATCGCAATG 1559
Db 1501 ATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCGATCGAGCTGATCGACATG 1560

QY 1560 GTCCATTACCTGTTTCATGTGCGGAGACCCGGGACCGGAAGTGGTCCCAACAGTCCAAGCA 1619
Db 1561 GTCCATTACCTGTTTCATGTGCGGAGACCCGGGACCGGAAGTGGTCCCAACAGTCCAAGCA 1620

QY 1620 GGTACGACAAAAGTCTGTCTGGGACCAACTCCCGGAGGCTACGAGAACCCCGGGGCCCA 1679
Db 1621 GGTACGACAAAAGTCTGTCTGGGACCAACTCCCGGAGGCTACGAGAACCCCGGGGCCCA 1680

QY 1680 AGTCCAGAGCCCGGCCAAACGTGCTCGAAATCGAGTGGTCCGAAGCAGCATTTTCCAAGG 1739
Db 1681 AGTCCAGAGCCCGGCCAAACGTGCTCGAAATCGAGTGGTCCGAAGCAGCATTTTCCAAGG 1740

QY 1740 AGTCCGAGCGCGCTCTATGGGCTGAACAGATCTCATCATCTGGGTTTCGGCGCTCAGAAC 1799
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Db 1741 AGCTCCGAGCGCGTCTATGGGCTGACGATCTCATCACACTGGGTTCGGCGCTCAGAAC 1800  
QY 1800 GCCGTTCAAGTGTGTTTCATTTTCGTTGGAACGGAGAGCTCTTTAGTTTGGAAAGGGTATAT 1859  
Db 1801 GCCGTTCAAGAGTGTTCATTTTCGTTGGAACGGAGAGCTCTTTAGTTTGGAAAGGGTATAT 1860  
QY 1860 GGAAGGGCCATAGATCGGTCGAGTCAACGAGTGTGTCAGAGAGTTGTGGCTAGCCTGGTGCC 1919  
Db 1861 GGAAGGGCCATAGATCGGTCGAGTCAACGAGTGTGTCAGAGAGTTGTGGCTAGCCTGGTGCC 1920  
QY 1920 AGCAGCATAG 1929  
Db 1921 AGCAGCATAG 1930

RESULT 4

US-09-352-159-43  
; Sequence 43, Application US/09352159A  
; Patent No. 6211434  
; GENERAL INFORMATION:  
; APPLICANT: Duwick, Jonathan P.  
; APPLICANT: Gilliam, Jacob T.  
; APPLICANT: Maddox, Joyce R.  
; TITLE OF INVENTION: Amino Polylamine Oxidase  
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use  
; FILE REFERENCE: 1134  
; CURRENT APPLICATION NUMBER: US/09/352,159A  
; EARLIEST FILING DATE: 1999-07-12  
; EARLIER APPLICATION NUMBER: 60/092,936  
; EARLIER FILING DATE: 1998-07-25  
; EARLIER APPLICATION NUMBER: 60/135,391  
; EARLIER FILING DATE: 1999-05-21  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 1928  
; TYPE: DNA  
; ORGANISM: Rhinocliadiella atrovirens  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (739)...(811)  
; NAME/KEY: Intron  
; LOCATION: (1134)...(1186)  
US-09-352-159-43

Query Match 92.9%; Score 1792.2; DB 4; Length 1928;  
Best Local Similarity 95.9%; Pred. No. 0;  
Matches 1850; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 1 ATGGCAGCTTGACCCGAGCTACATCAATCCCAACGTCGCTCCCAAGCAGGATATTC 60  
Db 1 ATGGCAGCTTGACCCGAGCTACATCAATCCCAACGTCGCTCCCAAGCAGGATATTC 60  
QY 61 CACATCGGCTAGGCCCCAAAGAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120  
Db 61 TACGTCGGCGTAGGCCCAACGAGGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120  
QY 121 GAGCGTTTGGGCGTGACAGACCCAGCTACGAGAACAGGTTGCCCAAGCATTCGCCAAT 180  
Db 121 GAGCGTTTGGGCGTGACAGACCCAGCTACGAGAACAGGTTGCCCAAGCATTCGCCAAT 180  
QY 181 CTGCGAGCTTGCTGTGCTGAGCTCTTCAACAGCAGCTCACCAGCTCAATTTAC 240  
Db 181 CTGCGAGCTTGCTGTGCTGAGCTCTTCAACAGCAGCTTACCAAGCATTTACCAATTTAC 240  
QY 241 TACATCGTCACTAGCCCCAGCAGCAAACTACCCCAATTTGAGATGGGCTGAAGTCTACC 300  
Db 241 TACATCGTCACTAGCAACCCAGCAGCAAACTACCCCAATTTGAGATGGGCTGAAGGCTACC 300  
QY 301 TTTCGCTTGACAGGCTCCCTCTTGCAGCTGGTGCCAGTACCAGGCTTGCTTCACCT 360  
Db 301 TTTCGCTTGACAGGCTCCCTCTTGCAGCTGGTGCCAGTACCAGGCTTGCTTCACCT 360

QY 361 GAATACCTCTTTAGGTTGATGCCACGCGCTGGTCCAGGACACTCGACCCCGAGAAC 420  
Db 361 GAATACCTCTTTAGGTTGATGCCACGCGCTGGTCCAGGACACTCGACCCCGAGAAC 420  
QY 421 GTTGGCAGCTGTAGTGGTGGGCGCTGGCTGTAGCGGTTTGGAGACGCGCAAGATC 480  
Db 421 GTTGGCAGCTGTAGTGGTGGGCGCTGGCTGTAGCGGTTTGGAGACGCGCAAGATC 480  
QY 481 CAGGCGCGCGGCTGTCTCTGCTCGCTCTTGTGAGCGATGGATCGGTAGGCGGAAAGACT 540  
Db 481 CAGGCTGCGCGGCTGTCTCTGCTCGCTCTTGTGAGCGATGGATCGGTAGGCGGAAAGACT 540  
QY 541 CTGAGCGTACAATCGGTCGCCGCGAGGAGCTATCAACGACCTCGGCGCTGCGTGGATC 600  
Db 541 CTGAGCGTACAATCGGTCGCCGCGAGGAGCTATCAATGACCTCGGCGCTGCGTGGATC 600  
QY 601 AATGACGACCAACGAAGATATCCAGATTTGTTGAAAGATTTTCATTTGAGGGCGAG 660  
Db 601 AATGACGACCAACGAAGATATTCAAATTTATTTGAAAGATTTTCATTTGAGGGCGAG 660  
QY 661 CTCCAGGACGACCGGAAATTCATCCATCAAGCACAGCGGTACACCACTACAGCT 720  
Db 661 CTCCAGGACGACCGGAAATTCATCCATCAAGCACAGCGGTACACCACTACAGCT 720  
QY 721 CCTTATGTTGACTCCCGGTAAGCAATCCCACTTTGTGATGAGACCTCTCTGCTGAGTGT 780  
Db 721 CCTTATGTTGATCCCTGTTAAGCAATTCATCTGTGATGAGACCTCTCTGCTGAGTGT 780  
QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCAGTTGC 840  
Db 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCAGTTGC 840  
QY 841 GGAACCTCTCCCGTATGCTCTCAGCTGATCGAAGAGTATAGCTTGAAGACCCCAAGGC 900  
Db 841 GGAACCTCTCCCGCATGCTCAGCTGATCGAAGAGTATAGCTTGAAGACCCCAAGGC 900  
QY 901 GAGCCCTCAGGCGAAGCGCTGCACAGTGTGAGCTTCGCGCACACTACTGTGAGAAGSACT 960  
Db 901 GAGCCCTCAGGCGAAGCGCTGCACAGTGTGAGCTTCGCGCACACTACTGTGAGAAGSACT 960  
QY 961 AAATTTGCTGCTGTTCTCAGCGTGCACCAACAGATCACACGGCTCTCTCGGTGTGA 1020  
Db 961 AAATTTGCTGCTGTTCTCAGCGTGCACCAACAGATCACACGGCTCTCTCGGTGTGA 1020  
QY 1021 AGCCACGAGATCAGCATGCTTTTCTCACCAGTACTACATCAAGAGTGCACCGGCTCAG 1080  
Db 1021 AGCCACGAGATCAGCATGCTTTTCTCACCAGTACTACATCAAGAGTGCACCGGCTCAG 1080  
QY 1081 TAATATTGCTCGGACAAGAACGCGCGGCGAGTATATGCGATGCAAAACAGGTGCGGTG 1140  
Db 1081 TAATATTGCTCGGATAAAGAACGCGTGGCGAGTATATGCGATGCAAAACAGGTGCGGTG 1140  
QY 1141 CGGTGCTCTCAGTAGGAGCTCGTTTCTTAGTGTCTATTCAGGTATCCAGTATGCAATTT 1200  
Db 1141 TGGTGTCTCTCA-GTGGAGACTCGTTTCTTAGTGTCTATTCAGGTATGCAATTT 1199  
QY 1201 TGCCATGCCATGTCAAGGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTGCC 1260  
Db 1200 TGCCATGCCATGTCAAGGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTGCC 1259  
QY 1261 GGAATTGAGCAGTCCGCGTCCGCTGTATAGTACGATCGGCTCGGGCGGCTGTTCCGA 1320  
Db 1260 GAAATTGAGCAGTCCGCTCCGCTGTACAGTACGATCGGCTCGGGCGGCTGTTCCGA 1319  
QY 1321 AGCAAAAGGTGGTGTTCGTTACCGACACATTTGATCCACCTTGACATTTTCACCA 1380  
Db 1320 AGTAAAAGGTGGTGTTCGTTACCGACACCTTTGATCCACCTTGATATTTTCACCA 1379  
QY 1381 CCTCTTCCCGCGGAGAGCAAGCATTTGGCGGAAATTTCTATCTCGGCTACTATAGCAAG 1440  
Db 1380 CCTCTTCCCGCGGAGAGCAAGCATTTGGCTGAAAAATCCATCTCTGGGCTACTATAGCAAG 1439

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QY 1441 ATAGCTTCGTATGGGACAAACCGGTGTGGCGGGAACAAGGCTTCGGGCGTCTCCCAA 1500
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Db 1440 ATAGCTTCGTATGGGACAAACCGGTGTGGCGGGAACAAGGCTTCGGGCGTCTCCCAA 1499
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QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGTCGAAAGTCGATCGGCAATGG 1560
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QY 1561 TCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAAGCAG 1620
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Db 1800 CCGTTCNAAGGTTCTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGGATATG 1859
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Db 1860 GAAGGGCCATACGATCGGGTCAACAGGTGCTGCAAGAGTTGTGGCTAGCGTGGTGC 1919
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QY 1921 GCAGCATAG 1929
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RESULT 5
US-09-352-159-45
; Sequence 45, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duivick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 1928
; TYPE: DNA
; ORGANISM: Rhinocladella atrovirens
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (739)...(811)
; NAME/KEY: Intron
; LOCATION: (1134)...(1185)
; US-09-352-159-45

Query Match 92.7%; Score 1789; DB 4; Length 1928;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

QY 1 ATGGCAGCTTGACCGAGCTACATCAATCCCCCAACCTCGCCTCCCCAGAGGGTATTCC 60
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Db 421 GTTCGGGACGCTGAGTGGGCGCTGGCTTGAAGGCTTTGGAGAGCGGCACGAAAGTC 480
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QY 1081 TAATATTTCTCGGACAAAGAAAGCGGGCAGTATATGCGATGCAAAACAGAGTGCCTG 1140
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QY 541 CTGAGCTAGCAATCGGGTCCCGCAGGACGACTATCAAGACCTCGGCGCTCGGTGGATC 600  
Db 541 CTGAGCTAGCAATCGGGTCCCGCAGGACGACTATCAAGACCTCGGCGCTCGGTGGATC 600  
QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATCTGTTTGAAGATTTTCATTTGAGGGCGAG 660  
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Db 735 -----CTTGCTGAGGAGGAGTTGCAAGTCACTTGC 767  
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Db 768 GGAATCCTCCCGTATGCTTCAGCTGATCGAAGATATAGCCTTGAAGACCCCAAGG 827  
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QY 1081 TAATATTGTCFCGACAGAAAGCGGCGAGTATATCGGATGCAAAACAGTGCCTG 1140  
Db 1008 TAATATTGTCFCGACAGAAAGCGGCGAGTATATCGGATGCAAAA----- 1057  
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Db 1058 -----CAGTATGCACTGAT 1074  
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Db 1075 TGCCATGCCATGTCAAAGGAATTTGTTCCAGGCTCAGTGCACCTCAACACCCCGCTGCT 1134  
QY 1261 GGAATTGACAGTCCGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGGCTGTTCCGA 1320  
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QY 1921 GCAGCATAG 1929  
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RESULT 8  
US-09-352-168-22  
; Sequence 22, Application US/09352168A  
; Patent No. 6211435  
; GENERAL INFORMATION:  
; APPLICANT: Crasta, Oswald R.  
; APPLICANT: Duvick, Jonathan P.  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Gilliam, Jacob T.  
; APPLICANT: Maddox, Joyce R.  
; TITLE OF INVENTION: Amino Polyol Amine Oxidase  
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use  
; FILE REFERENCE: 0875  
; CURRENT APPLICATION NUMBER: US/09/352,168A  
; CURRENT FILING DATE: 1999-07-12  
; EARLIER APPLICATION NUMBER: 60/092,936  
; EARLIER FILING DATE: 1998-07-25  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 1803  
; TYPE: DNA  
; ORGANISM: Exophiala spinifera  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1800)  
US-09-352-168-22  
  
Query Match 83.1%; Score 1602.6; DB 4; Length 1803;  
Best Local Similarity 91.7%; Pred. No. 0;  
Matches 1769; Conservative 0; Mismatches 34; Indels 126; Gaps 2;  
  
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QY 241 TACATCGTCGACTACGCCCGAGCAAACTCACCGCAATTTGAGATGGGCTGAAGTCTACC 300
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Db 1735 GAAGGGCCATACGATCGGTCACAGAGTGTCTCGAAGTGTGTGGCTAGCGTGGTGCCA 1794
QY 1921 GCAGCATAG 1929
Db 1795 GCAGCATAG 1803

RESULT 9
US-09-352-159-32
; Sequence 32, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 2490
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: GST:glyc(-)APAO open reading frame, 2490 nt; GST
; OTHER INFORMATION: and linker, nt 1-687; glyc (-) APAO, nt 688-2490;
; OTHER INFORMATION: mutation in putative glycosylation sites, nt
; OTHER INFORMATION: 1288-1290 (AAT-> TCC) and nt 1303-1305 (AGC->AAC).
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (1)...(2487)
; NAME/KEY: misc_feature
; LOCATION: (1)...(687)
; OTHER INFORMATION: GST and linker
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; LOCATION: (688)...(2490)
; OTHER INFORMATION: Glyc (-) APAO
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1288)...(1290)
; OTHER INFORMATION: mutation in putative glycosylation site (AAT->TCC)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1303)...(1305)
; OTHER INFORMATION: mutation in putative silycosylation site (AGC->AAC)
; US-09-352-159-32

Query Match      82.7%; Score 1596.2; DB 4; Length 2490;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;

QY 1 ATGCGACCTTGACCGAGCTACATCAATCCCCAAAGCTGCGCTCCCCAGCAGGGTATTC 60
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DB 748 CACATCGGGTAGGCCCAACAGAGGAGGTATGTGACATAGCTGGACAGATGGACAA 807
QY 121 GACGCTTTGGGCGTGACAGACCCAGCGCTACGAGAAACAGGTTGCCAAAGCATTCGCAAT 180
DB 808 GACGCTTTGGGCGTGACAGACCCCTGCTCTACGAGAAACAGGTTGCCAAAGCATTCGCAAT 867
QY 181 CTGCGAGCTTGCCCTTGCTGCACTTGGAGCCTCTTCAACAGACGTCAACAGCTCAATTAC 240
DB 868 CTGCGAGCTTGCCCTTGCTGCACTTGGAGCCACTTCAACAGACGTCAACAGCTCAATTAC 927
QY 241 TACATCGTCGACTACGCCCGGAGCAAACTCACCGCAATTTGGAGATGGCTGAAGTCTACC 300
DB 928 TACATCGTCGACTACGCCCGGAGCAAACTCACCGCAATTTGGAGATGGCTGAAGTCTACC 987
QY -301 TTGCGCCTTGACAGGCTCCCTCCCTTGACGCTGGTGCCAGTACCGGCGCTTGGCTTCACCT 360
DB 988 TTGCGCCTTGACAGGCTCCCTCCCTTGACGCTGGTGCCAGTACCGGCGCTTGGCTTCACCT 1047
QY 361 GAATACCTCTTTAGGTTGATGCCACGCGCTGGTGCCAGACACTCGACCCAGACAAAC 420
DB 1048 GAATACCTCTTTAGGTTGATGCCACGCGCTGGTGCCAGACACTCGACCCAGACAAAC 1107
QY 421 GTTGGGACGTTGAGTGGTGCGGCTGGCTTGGAGCGGTTTGGAGCGGCAAGAGTC 480
DB 1108 GTTGGGACGTTGAGTGGTGCGGCTGGCTTGGAGCGGTTTGGAGCGGCAAGAGTC 1167
QY 481 CAGGCGCGGCTGCTGCTGCTGCTGCTTGGAGCGATGGATCGTGTAGGGGGAAGACT 540
DB 1168 CAGGCGCGGCTGCTGCTGCTGCTGCTTGGAGCGATGGATCGTGTAGGGGGAAGACT 1227
QY 541 CTGACGCTACAAATCGGGTCCCGGAGGACGACTATCAACGACCTTCGGGCTGCGTGATC 600
DB 1228 CTGACGCTACAAATCGGGTCCCGGAGGACGACTATCAACGACCTTCGGGCTGCGTGATC 1287
QY 601 AATGACGACCAACCAAGCAAGTATCCAGATTGTTGAAAGATTTCATTTGGAGGGCGAG 660
DB 1288 TCCGACGACCAACCAAGCAAGTATCCAGATTGTTGAAAGATTTCATTTGGAGGGCGAG 1347
QY 661 CTCCAGAGGACGACCGGAAATTCATTCATCAAGCACAAGACGGTACAAACACTACAGCT 720
DB 1348 CTCGAGAGGACGACTGGAATTCATTCATCAAGCACAAGACGGTACAAACACTACAGCT 1407
QY 721 CCTTATGGTACTCCCGGTAAAGCAATCCCACTTTGTGTATGAGACCTCTGTGAGTGT 780
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DB 1408 CCTTATGGTGACTC----- 1421
QY 781 AGAATACAGTCACTGACTCCACTTCGCTCCAGCTGAGCGAGAGGTTGCAAGTGCACCTTGC 840
DB 1422 -----CTTGCTGAGCGAGGAGGTTGCAAGTGCACCTTGC 1454
QY 841 GGAATCCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900
DB 1455 GGAATCCTCCCGTATGGTCTCAGCTGATCGAAGAGCATAGCCTTCAAGACCTCAAGGC 1514
QY 901 GAGCCCTCAGCGGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT 960
DB 1515 GAGCCCTCAGCGGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGAACT 1574
QY 961 AAACCTTGCTGCTGCTCAGCGTGGCAAAACAGATCACACGCGCTCTGCTGCGTGTGGA 1020
DB 1575 AAACCTTGCTGCTGCTGCTGCGGTAGCAAAACAGATCACACGCGCTCTGCTGCGTGTGGA 1634
QY 1021 AGCCCAACGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1080
DB 1635 AGCCCAACGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1694
QY 1081 TAAATATTGCTCGGACAAGAAGACGGCGGCGAGTATATGCGATGCAAAA 1140
DB 1695 TAAATATTGCTCGGACAAGAAGACGGCGGCGAGTATATGCGATGCAAAA 1744
QY 1141 CGGTGCTCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCAATTCAGGATGACGTCGATT 1200
DB 1745 -----CAGGTATGCGATGCGATT 1761
QY 1201 TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTCTCCT 1260
DB 1762 TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTCTCCT 1821
QY 1261 GGAATTTGACGACTCGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCGA 1320
DB 1822 GAAATTTGACGACTCGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCGA 1881
QY 1321 AGCAAAAAGCTGGTGGTTTCTTACCGACAACATTTGTATCCACCTTGACATTTTCAACA 1380
DB 1882 AGCAAAAAGCTGGTGGTTTCTTACCGACAACCTTTGTATCCACCTTGACATTTTCAACA 1941
QY 1381 CTTCTTCCCGCGGAGAACGACATTTGGCGGAAAAATCTATCTCGGCTTATAGCAAG 1440
DB 1942 CTTCTTCCCGCGGAGAACGACATTTGGCGGAAAAATCTATCTCGGCTTATAGCAAG 2001
QY 1441 ATAGTCTTCTGATGGACAACCGCTGCTGGCGCAACAAGGCTTCTCGGCGCTCTCCAA 1500
DB 2002 ATAGTCTTCTGATGGACAACCGCTGCTGGCGCAACAAGGCTTCTCGGCGCTCTCCAA 2061
QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGATACAGATCGAAGTCTGCGCAATGG 1560
DB 2062 TCGAGCTGTGACCCCATCTCATTTGCCAGATACAGATCGAAGTCTGCGCAATGG 2121
QY 1561 TCATTTACCTGTTTCATGGTCGGAGACCGGAGAGTGTGCTCCCAACAGTCCCAAGCAG 1620
DB 2122 TCATTTACCTGTTTCATGGTCGGAGACCGGAGAGTGTGCTCCCAACAGTCCCAAGCAG 2181
QY 1621 GTACGACAAAAGTCTGCTCTGGGACCAACTCCGCGCAACCTACGAGAACCCCGGGGCCAA 1680
DB 2182 GTACGACAAAAGTCTGCTCTGGGACCAACTCCGCGCAACCTACGAGAACCCCGGGGCCAA 2241
QY 1681 GTCCAGAGCGGCCCAACGCTGCTCGAAATCGAGTGTGCAAGCAGCAGTATTTCCAAAG 1740
DB 2242 GTCCAGAGCGGCCCAACGCTGCTCGAAATCGAGTGTGCAAGCAGCAGTATTTCCAAAG 2301
QY 1741 GCTCCGAGCGCGCTATGGCTGACGATCTCATCACACTGGGTTCGGGCTCAGAAGC 1800
DB 2302 GCTCCGAGCGCGCTATGGCTGACGATCTCATCACACTGGGTTCGGGCTCAGAAGC 2361
QY 1801 CCGTTCAAGTGTCTCATTTTCGTTGGAACGAGACGCTCTTTAGTTTGGAAAGGCTATATG 1860
DB 2362 CCGTTCAAGTGTCTCATTTTCGTTGGAACGAGACGCTCTTTAGTTTGGAAAGGCTATATG 2421
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QY 1861 GAAGGGCCATACGATCGGTCAACGAGGTGCTGCAGAGTTGTGGCTAGCCTGGTGCCA 1920  
|||||  
Db 2422 GAAGGGCCATACGATCGGTCAACGAGGTGCTGCAGAGTTGTGGCTAGCCTGGTGCCA 2481  
|||||

QY 1921 GCAGCATAG 1929  
|||||  
Db 2482 GCAGCATAG 2490  
|||||

## RESULT 10

US-09-352-168-32

; Sequence 32, Application US/09352168A

; Patent No. 6211435

; GENERAL INFORMATION:

; APPLICANT: Crasta, Oswald R.

; APPLICANT: Duvick, Jonathan P.

; APPLICANT: Folkerts, Otto

; APPLICANT: Gilliam, Jacob T.

; APPLICANT: Maddox, Joyce R.

; TITLE OF INVENTION: Amino Polyol Amine Oxidase

; FILE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use

; FILE REFERENCE: 0875

; CURRENT APPLICATION NUMBER: US/09/352,168A

; CURRENT FILING DATE: 1999-07-12

; EARLIER APPLICATION NUMBER: 60/092,936

; EARLIER FILING DATE: 1998-07-25

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 32

; LENGTH: 2490

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: GST:glyc(-)APAO open reading frame, 2490 nt; GST

; OTHER INFORMATION: and linker, nt 1-687; Glyc (-) APAO, nt 688-2490;

; OTHER INFORMATION: mutation in putative glycosylation sites in bold

; OTHER INFORMATION: and underlined, nt 1288-1290 (AAT-&gt; TCC) and nt

; OTHER INFORMATION: 1303-1305 (AGC-&gt; AAC).

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2487)

; NAME/KEY: misc\_feature

; LOCATION: (1)...(687)

; OTHER INFORMATION: GST and linker

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (688)...(2490)

; OTHER INFORMATION: Glyc (-) APAO

; FEATURE:

; NAME/KEY: mutation

; LOCATION: (1288)...(1290)

; OTHER INFORMATION: mutation in putative glycosylation site (AAT-&gt;TCC)

; FEATURE:

; NAME/KEY: mutation

; LOCATION: (1303)...(1305)

; OTHER INFORMATION: mutation in putative glycosylation site (AGC-&gt;AAC)

; US-09-352-168-32

## Query Match

Best Local Similarity 82.7%; Score 1596.2; DB 4; Length 2490;

Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;

QY 1 ATGGCAGCTGCACGAGCTACATCAATCCCGCAACCTCGCTCCCGCAGGAGTATTC 60

Db 688 ATGGCAGCTGCACGAGCTACATCAATCCCGCAACCTCGCTCCCGCAGGAGTATTC 747

QY 61 CACATCGCGGTAGCCCAAGCAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120

Db 748 CACGTGCGGTAGCCCAAGCAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 807

QY 121 GACGCTTTGGCGTGACAGACCCAGCCTACGAGAAACAGGTGCCCAAGCATTCGCAAT 180

|||||

Db 808 GACGCTTCGGGCGTGACAGACCCCTGCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 867  
QY 181 CTGGAGCTTCCTTGTGAGTTGGAGCTCTTTCAAAGACGCTACCAAGCTCAATTAC 240  
Db 868 CTGGAGCTTCCTTGTGAGTTGGAGCTCTTTCAAAGACGCTACCAAGCTCAATTAC 927  
QY 241 TACATCGTGCAGTACGCCCGGAGCAAACTCACCGCAATTTGGAGATGGGTGAAGTCTACC 300  
Db 928 TACATCGTGCAGTACGCCCGGAGCAAACTCACCGCAATTTGGAGATGGGTGAAGTCTACC 987  
QY 301 TTTGCCCTTGACAGCTCCCTCTTGACACCTGCTGCACGCTACCGGCTTTGGCTTCACCT 360  
Db 988 TTTGCCCTTGACAGCTCCCTCTTGACACCTGCTGCACGCTACCGGCTTTGGCTTCACCT 1047  
QY 361 GAATACCTCTTTGAGTTGATGCCACGGCTGCTGCCAGACACTCGACCCCGAGACAAC 420  
Db 1048 GAATACCTCTTTGAGTTGATGCCACGGCTGCTGCCAGACACTCGACCCCGAGACAAC 1107  
QY 421 GTTGGGACGTGTAGTGGTGGGCTGCTGAGCGGTTTGGAGACGCGCACGCAAGTC 480  
Db 1108 GTTGGGACGTGTAGTGGTGGGCTGCTGAGCGGTTTGGAGACGCGCACGCAAGTC 1167  
QY 481 CAGCCCGCGTCTGCTCTGCTGCTGCTTTGAGCGGATGATCGTGTAGGGGAAAGACT 540  
Db 1168 CAGCCCGCGTCTGCTCTGCTGCTTTGAGCGGATGATCGTGTAGGGGAAAGACT 1227  
QY 541 CTGAGCGTACAAATCGGCTCCCGGAGGACACTATCAACGACCTCGGCGCTGGTGGATC 600  
Db 1228 CTGAGCGTACAAATCGGCTCCCGGAGGACACTATCAACGACCTCGGCGCTGGTGGATC 1287  
QY 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGCGGAG 660  
Db 1288 TCCGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGCGGAG 1347  
QY 661 CTCAGAGGAGCAGCGGAATTCATCCATCAAGCACAGACGGTACACCACACTACAGCT 720  
Db 1348 CTCAGAGGAGCAGCGGAATTCATCCATCAAGCACAGACGGTACACCACACTACAGCT 1407  
QY 721 CTTTATGTGTACTCCCGGTAAAGCACAAATCCCACTTTGTGATGAGACCTCTGTGAGTGT 780  
Db 1408 CTTTATGTGTACTC----- 1421  
QY 781 AGAATACAGTCACTGACTCCACTTCGCTCAGCTGAGGAGGAGGTTGCAAGTGCACTTGC 840  
Db 1422 -----CTTGTCTGAGCGAGGAGTTGCAAGTGCACTTGC 1454  
QY 841 GGAATCTCTCCCGTATGCTCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGC 900  
Db 1455 GGAATCTCTCCCGTATGCTCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGC 1514  
QY 901 GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTGGCGCACTACTGTGAGAGGACCT 960  
Db 1515 GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTGGCGCACTACTGTGAGAGGAACT 1574  
QY 961 AAATTTGCTCTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTGGTGTGA 1020  
Db 1575 AAATTTGCTCTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTGGTGTGA 1634  
QY 1021 AGCCACAGATCAGCATGCTTTTCTCACCAGTACATCAAGAGTGCCACCGGTTCTCAG 1080  
Db 1635 AGCCACAGATCAGCATGCTTTTCTCACCAGTACATCAAGAGTGCCACCGGTTCTCAG 1694  
QY 1081 TAATATTTCTCGACAAAGAACGCGGCGAGTATATCGATGCAAAACAGTCCGCTG 1140  
Db 1695 TAATATTTCTCGACAAAGAACGCGGCGAGTATATCGATGCAAAACAGTCCGCTG 1744  
QY 1141 CGGTGTCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCAATTCAGGTATGCAAGTCGATT 1200  
Db 1745 -----CAGGTATGCAAGTCGATT 1761  
QY 1201 TGCCATGCCATGTCAAAGGAACTTTTCCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260  
Db 1762 TGCCATGCCATGTCAAAGGAACTTTTCCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1821

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QY 1261 GGAATTGAGCAGTCGGGCTCCGCTGTATAGTACGATCGSCCTCGGCGCGCTGTCCGA 1320
Db 1822 GAAATTGAGCAGTCGGGATCCGGCTGTACAGTACGATCGGCCCTCGGGCGCGGTGCCGA 1881
QY 1321 AGCAAAAAGGTGGTGGTTTCGTTACCGACAAACATTGTATCCCACTTGACATTTTCACCA 1380
Db 1882 AGCAAAAAGGTGGTGGTTTCGTTACCGACAAACCTTGTATCCCACTTGACATTTTCACCA 1941
QY 1381 CCTCTTCCCGCGAGAACGATTTGGCGGAAAAATCTATCTCCGTCTACTATACGAG 1440
Db 1942 CCTCTTCCCGCGAGAACGATTTGGCGGAAAAATCTATCTCCGTCTACTATACGAG 2001
QY 1441 ATAGTCTTCGTATGGGACAAACCGTGTGGCGGACAAAGGCTTCTCGGGCGTCTCCAA 1500
Db 2002 ATAGTCTTCGTATGGGACAAACCGTGTGGCGGACAAAGGCTTCTCGGGCGTCTCCAA 2061
QY 1501 TCGAGCTGTGACCCCATCTCATTTGGCAGAGATACCAAGCATCGAAATCGATCGGCAATGG 1560
Db 2062 TCGAGCTGTGACCCCATCTCATTTGGCAGAGATACCAAGCATCGAGCTCGATCGACAATGG 2121
QY 1561 TCCATTACCTGTTTCATGTCGGAGACCCGGGAGGAGTGGTCCCAACAGTCCAAAGCAG 1620
Db 2122 TCCATTACCTGTTTCATGTCGGAGACCCGGGAGGAGTGGTCCCAACAGTCCAAAGCAG 2181
QY 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCGCGCAGCCTACGAGAACGCCGGGGCCCAA 1680
Db 2182 GTACGACAAAAGTCTGTCTGGGACCAACTCGCGCAGCCTACGAGAACGCCGGGGCCCAA 2241
QY 1681 GTCCAGAGCGGGCCAAACGTCTCGAAATCGAGTGGTCTGAGAGCAGCAGTATTTCCAAAGGA 1740
Db 2242 GTCCAGAGCGGGCCAAACGTCTCGAAATCGAGTGGTCTGAGAGCAGCAGTATTTCCAAAGGA 2301
QY 1741 GCTCGGAGCGCGTCTATGGGCTGAACGATCTCATCAGTGGTTCGGGCGCTCAGAACG 1800
Db 2302 GCTCGGAGCGCGTCTATGGGCTGAACGATCTCATCAGTGGTTCGGGCGCTCAGAACG 2361
QY 1801 CCGTTCAGTGTGTTTCATTTTCGTTGGAACGAGACGCTCTTAGTTTGGAAAGGCTATATG 1860
Db 2362 CCGTTCAGAGTGTTCATTTTCGTTGGAACGAGACGCTCTTAGTTTGGAAAGGCTATATG 2421
QY 1861 GAAGGGGCCATACGATCGGGTCAACAGAGGCTCTGCAGAAAGTGTGGTCTAGCTGGTGCCA 1920
Db 2422 GAAGGGGCCATACGATCGGGTCAACAGAGGCTCTGCAGAAAGTGTGGTCTAGCTGGTGCCA 2481
QY 1921 GCAGCATAG 1929
Db 2482 GCAGCATAG 2490
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RESULT 11

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US-09-352-159-7
; Sequence 7, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: DuVick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Exophiala spinifera
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(646)
; NAME/KEY: Intron
; LOCATION: (647)...(699)
; NAME/KEY: CDS
; LOCATION: (700)...(1439)
US-09-352-159-7
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Query Match 68.4%; Score 1319; DB 4; Length 1442;

Best Local Similarity 93.5%; Pred. No. 0;

Matches 1417; Conservative 0; Mismatches 25; Indels 73; Gaps 1;

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QY 415 GACAAAGTTGCGGACGTGGTAGTGGTGGCGCTGGCTTTGAGCGGTTTGAGACGCGCACGC 474
Db 1 GACACAGTTGCGGACGTGGTAGTGGTGGCGCTGGCTTTGAGCGGTTTGAGACGCGCACGC 60
QY 475 AAAGTCCAGGCGCGCGGTCTGTCTCGCTCGCTTTGAGGCGATGGATCGTGTAGGGGGA 534
Db 61 AAAGTCCAGGCGCGCGGTCTGTCTCGCTCGCTTTGAGGCGATGGATCGTGTAGGGGGA 120
QY 535 AAGACTCTGAGCGTACAATCGGGTCCCGGACGAGCACTATCAACGACCTCGGCGCTCGC 594
Db 121 AAGACTCTGAGCGTACAATCGGGTCCCGGACGAGCACTATCAACGACCTCGGCGCTCGC 180
QY 595 TGGATCAATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGAATTTTCATTTGGAG 654
Db 181 TGGATCAATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGAATTTTCATTTGGAG 240
QY 655 GCGGAGCTCCAGAGACGACCGGAAATTCATTCATCAAGCAACAGACGGTACACCACT 714
Db 241 GCGGAGCTCCAGAGACGACCTGGAATTCATTCATCAAGCAACAGACGGTACACCACT 300
QY 715 ACAGCTCCCTTATGTTGATGACCTCCCGGTAAAGCAACATCCCACTTTGTGATGAGACCTCTGTC 774
Db 301 ACAGCTCCCTTATGTTGATGACCTCCCGGTAAAGCAACATCCCACTTTGTGATGAGACCTCTGTC 320
QY 775 GAGTGTAGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGC 834
Db 321 -----CTTGCTGAGCGAGGAGTTGCAAGTGC 347
QY 835 ACTTGGGAACTCCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCC 894
Db 348 ACTTGGGAACTCCTCCCGTATGGTCTCAGCTGATCGAAGAGCATAGCTTCAAGACCT 407
QY 895 CAAGCGAGCCCTCAGCGAAGCGGCTGCACAGTGTGAGCTTCGGCGCACTACTGTGAGAA 954
Db 408 CAAGCGAGCCCTCAGCGAAGCGGCTGCACAGTGTGAGCTTCGGCGCACTACTGTGAGAA 467
QY 955 GGACCTAAACTTGCCTGCTTCTCAGCGTGGCAACCAAGATCACACGCGCTCTGCTCGG 1014
Db 468 GGAACCTAAACTTGCCTGCTTCTCAGCGCTAGCAAAACCAAGATCACACGCGCTCTGCTCGG 527
QY 1015 TGTGGAAGCCACGATCAGCATGCTTTCTCACCAGTACATCAAGAGTGCACCGG 1074
Db 528 TGTGGAAGCCACGATCAGCATGCTTTCTCACCAGTACATCAAGAGTGCACCGG 587
QY 1075 TCTCAGTAAATATTTCTCGGACAAAGAACGCGGCGCAGTATATCGGATGCAAAAACAG 1134
Db 588 TCTCAGTAAATATTTCTCGGACAAAGAACGCGGCGCAGTATGCGGATGCAAAAACAG 647
QY 1135 TGGTGGGTTGCTCCTCAGGTAGGGGACTCGTTTCTTAGTGGTCAATCCAGGTATGCAAG 1194
Db 648 TGGTGGTGGTGTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCAATCCAGGTATGCAAG 707
QY 1195 TCGATTTGCCATGCCATGTCAAAGAACTTTGTTCCAGGCTCAGTCACCTCAACACCCGCC 1254
Db 708 TCGATTTGCCATGCCATGTCAAAGAACTTTGTTCCAGGCTCAGTCACCTCAACACCCGCC 767
QY 1255 GTCGCTGGAATGAGCAGTCGGGCTCGGCTGTATAGTACGATCGGCGCGCGCTG 1314
Db 768 GTCGCTGGAATGAGCAGTCGGGCTCGGCTGTACAGTACGATCGGCGCGCGCTG 827
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Db 888 TCACCACTCTTCCCGCCGAGAGCAAGCATTTGGCGGAAAATTCATCTCGGCTACTAT 947
QY 1435 AGCAAGATAGTCTTCGTATGGGACAAACCGGTGGTGGCGGCAAAAGGCTTTCGGGGCGTC 1494
Db 948 AGCAAGATAGTCTTCGTATGGGACAAAGCGGTGGTGGCGGCAAAAGGCTTTCGGGGCGTC 1007
QY 1495 CTCGAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCCGATCGG 1554
Db 1008 CTCGAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCCGATCGA 1067
QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGGCGGAAGTGGTCCCAACAGTCC 1614
Db 1068 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGGCGGAAGTGGTCCCAACAGTCC 1127
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTACGAGAACGCCGGG 1674
Db 1128 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTACGAGAACGCCGGG 1187
QY 1675 GCCCAAGTCCAGAGCGGGCCAACTGCTCGAATCGAGTGGTCCGAAGCAGCATTTTC 1734
Db 1188 GCCCAAGTCCAGAGCGGGCCAACTGCTCGAATCGAGTGGTCCGAAGCAGCATTTTC 1247
QY 1735 CAAGGAGCTCCGAGCGCGCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1794
Db 1248 CAAGGAGCTCCGAGCGCGCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1307
QY 1795 AGAAGCGGTTCAAGTGTGTTTCATTTGTTGGAACGGAGACGCTTTAGTTGGAAAGGG 1854
Db 1308 AGAAGCGGTTCAAGTGTGTTTCATTTGTTGGAACGGAGACGCTTTAGTTGGAAAGGG 1367
QY 1855 TATATGAGGGGCCATACGATCGGTCACAGAGGTGCTCGAAGTGTGTCAGCCTG 1914
Db 1368 TATATGAGGGGCCATACGATCGGTCACAGAGGTGCTCGAAGTGTGTCAGCCTG 1427
QY 1915 GTGCCAGCAGCATAG 1929
Db 1428 GTGCCAGCAGCATAG 1442
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RESULT 13

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US-09-352-159-26
; Sequence 26, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Barley alpha amylase signal sequence: BEST1
; OTHER INFORMATION: mature: artificial spacer: and K:trAPAO. For
; OTHER INFORMATION: plant expression.
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(72)
; OTHER INFORMATION: Barley alpha amylase signal sequence
; FEATURE:
; NAME/KEY: mat_peptide
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; LOCATION: (73)...(1545)
; OTHER INFORMATION: BEST1 mature
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1546)...(1584)
; OTHER INFORMATION: spacer sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1585)...(2973)
; OTHER INFORMATION: K:trAPAO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2973)
; NAME/KEY: misc_feature
; LOCATION: (1585)...(1587)
; OTHER INFORMATION: Extra lysine
US-09-352-159-26

Query Match 62.8%; Score 1212.2; DB 4; Length 2976;
Best Local Similarity 90.2%; Pred. No. 0;
Matches 1372; Conservative 0; Mismatches 23; Indels 126; Gaps 2;

QY 409 ACCCCAGACAAGTTTCGGAGCATGTGTAGTGGGCGCTGGCTTGAGCGGTTTGGAGACG 468
Db 1582 AGCAAAAGACAACGTTTCGGAGCATGTGTAGTGGGCGCTGGCTTGAGCGGTTTGGAGACG 1641
QY 469 GCACGCAAAAGTCCAGCGCGGCTGTCTCTGCCCTCTTGTAGAGCGCATGGATCGTGTA 528
Db 1642 GCACGCAAAAGTCCAGCGCGGCTGTCTCTGCCCTCTTGTAGAGCGCATGGATCGTGTA 1701
QY 529 GGGGGAAGACCTCTGAGCGTACAATCGGTCGCCGAGGACGACTATCAAGCACTCCGCG 588
Db 1702 GGGGGAAGACCTCTGAGCGTACAATCGGTCGCCGAGGACGACTATCAAGCACTCCGCG 1761
QY 589 GCTGCGTGGATCAATGACAGCAACCAAGGATCCAGATCTGTTTGAAGATTTTCAT 648
Db 1762 GCTGCGTGGATCAATGACAGCAACCAAGGATCCAGATCTGTTTGAAGATTTTCAT 1821
QY 649 TTGGAGGGCGAGCTCCAGAGGACGACCGGAAATTCATCCATCAAGCAACAGCGGTACA 708
Db 1822 TTGGAGGGCGAGCTCCAGAGGACGACTGGAATTCATCCATCAAGCAACAGCGGTACA 1881
QY 709 ACCACTACAGCTCCTTATGTTGACTCCCGGTAAGCAACATCCCACTTTGTGATGAGACC 768
Db 1882 ACCACTACAGCTCCTTATGTTGACTC----- 1907
QY 769 TCTGTGAGTGTAGATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGGTTGC 828
Db 1908 -----CTTGTGAGCGAGGAGGTTGC 1928
QY 829 AAGTGCACTTGGGAACTCCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGA 888
Db 1929 AAGTGCACTTGGGAACTCCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGA 1988
QY 889 AGACCCCAAGGGAGCGCCCTCAGCGGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTG 948
Db 1989 AGACCTCAAGGGAGCGCCCTCAGCGGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTG 2048
QY 949 TGAGAAGGACCTAAACTTGCCTGCTCTCAGCGTGGCAACACAGATCACACGGGCTCT 1008
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QY 1009 GCTCGGTGTGGAAGCCAGAGATCAGCATGCTTTTCTCACCAGCTACATCAAGAGTGC 1068
Db 2109 GCTCGGTGTGGAAGCCAGAGATCAGCATGCTTTTCTCACCAGCTACATCAAGAGTGC 2168
QY 1069 CACCGGTCTCAGTAATATTGTCGCGACAAAGAACGGCGGCGAGTATATGCGATGCAA 1128
Db 2169 CACCGGTCTCAGTAATATTGTCGCGACAAAGAACGGCGGCGAGTATATGCGATGCAA 2228
QY 1129 AACAGGTGCGTGGGTCCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTTCATTCAGGT 1188
Db 2229 AA-----CAGGT 2235
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QY	1189	ATGCAGTCGATTTGCCATGCCATGTCAAAGAACTTGTTCACGGCTCAGTGCACCTCAAC	1248
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QY	1249	ACCCCGCTCGCTGGAATTGAGCAGTCGGGGTCCGGCTGTATAGTACGATCGGCCTCGGGC	1308
Db	2296	ACCCCGCTCGCTGGAATTGAGCAGTCGGCATCCGGCTGTACAGTACGATCGGCCTCGGGC	2355
QY	1309	GCCGTGTTCCGAGCAAAAAAGTGTTTCGTTTACCGACAACATCTGTATCCCAACCTTG	1368
Db	2356	GCCGTGTTCCGAGCAAAAAAGTGTTTCGTTTACCGACAACCTGTGTATCCCAACCTTG	2415
QY	1369	ACATTTTCAACCACTCTTCCGCCGAGAAAGCAAGCAATTCGGGGAAAAATCTATCCTCGGC	1428
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QY	1429	TACTATAGCAAGATAGTCTTCGTATGGGACAACCCGCTGGTGGCGCGCAACAAGGCTTCTCG	1488
Db	2476	TACTATAGCAAGATAGTCTTCGTATGGGACAAGCCGCTGGTGGCGCGCAACAAGGCTTCTCG	2535
QY	1489	GGCTCTCTCCAATCGAGCTGTGACCCCACTCTCATTTGCCAGAGATACCAGCATCGAAGTC	1548
Db	2536	GGCTCTCTCCAATCGAGCTGTGACCCCACTCTCATTTGCCAGAGATACCAGCATCGAAGTC	2595
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QY	1849	AAAGGGTATATGAAGGGGCCATACGATCGGGTCAACGAGTGCTCGAGAAGTTTGGCT	1908
Db	2896	AAAGGGTATATGAAGGGGCCATACGATCGGGTCAACGAGTGCTCGAGAAGTTTGGCT	2955
QY	1909	AGCCTGGTCCACGACGATAG	1929
Db	2956	AGCCTGGTCCACGACGATAG	2976

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RESULT 14
US-09-352-168-26
; Sequence 26, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FASTSEQ for Windows Version 3.0

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; SEQ ID NO 26
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; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Barley alpha amylase signal sequence: BEST1
; OTHER INFORMATION: mature: artificial spacer; and K:trAPAO. For
; OTHER INFORMATION: plant expression.
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(72)
; OTHER INFORMATION: Barley alpha amylase signal sequence.
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (73)..(1545)
; OTHER INFORMATION: BEST1 mature
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1546)..(1584)
; OTHER INFORMATION: Artificial spacer sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1585)..(2973)
; OTHER INFORMATION: K:trAPAO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2973)
; NAME/KEY: misc_feature
; LOCATION: (1585)..(1587)
; OTHER INFORMATION: Extra lysine
; US-09-352-168-26

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Query Match	62.8%;	Score 1212.2;	DB 4;	Length 2976;
Best Local Similarity	90.2%;	Pred. No. 0;		
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Qy	469	GCACGCAAGTCCAGGCGCGGCTGTCTCTGCTCGTCTTTGAGCGATGATCGTGTA	528	
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Qy	529	GGGGGAAGACTCTGACGCTACAAATCGGGTCCGGCAGGACGACTATCAACGACCTCGGC	588	
Db	1702	GGGGGAAGACTCTGACGCTACAAATCGGGTCCGGCAGGACGACTATCAACGACCTCGGC	176	
Qy	589	GCTGCGTGGATCAATGACACCAACCAAGATATCCAGATCTGTTGAAGATTTTCAT	648	
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Qy 829 AAGTGCACCTTGGGAACCTCCCGCTATGCTCTCAGCTGATCGAAGAGTATAGCCCTTGA 888  
Db 1956 AAGTGCACCTTGGGAACCTCCCGCTATGCTCTCAGCTGATCGAAGAGCATAGCCCTCA 2015  
Qy 889 AGACCCCAAGCGGAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTG 948  
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Qy 949 TGAGAAGGACCTTAAACTTGCCTGCTGTTCTCAGCGTGGCAAAACAGATCACACGCGCTCT 1008  
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Db 2256 AA-----CAGGT 2262  
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Qy 1669 GCGGGGCCCCAGTCCAGAGCCGCAACGCTCGAATCGAGTGGTGGAGCAGCAG 1728  
Db 2743 GCGGGGCCCCAGTCCAGAGCCGCAACGCTCGAATCGAGTGGTGGAGCAGCAG 2802  
Qy 1729 TATTTCCAGGAGCTCCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGGTTG 1788  
Db 2803 TATTTCCAGGAGCTCCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGGTTG 2862  
Qy 1789 GCGCTCAGAACCGGCTTCAAGTGTGTTTCATTTGTTGACGAGACGCTTTAGTTGG 1848  
Db 2863 GCGCTCAGAACCGGCTTCAAGAGTGTTCATTTGTTGACGAGACGCTTTAGTTGG 2922

Qy 1849 AAAGGGTATATGGAAGGGCCATACGATCGGTTCAACGAGGTGCTGCAGAAGTTGTGGCT 1908  
Db 2923 AAAGGGTATATGGAAGGGGCCATACGATCGGTTCAACGAGGTGCTGCAGAAGTTGTGGCT 2982  
Qy 1909 AGCCTGGTCCAGCAGCATAG 1929  
Db 2983 AGCCTGGTCCAGCAGCATAG 3003

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Job time : 96 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: November 12, 2002, 03:21:40 ; Search time 140 Seconds  
(without alignments)  
4888.437 Million cell updates/sec

Title: US-09-771-045A-35  
Perfect score: 1929  
Sequence: 1 atggcacttgaccagacta.....gcttgggtgccagcagcatag 1929

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	40.8	2.1	2491	10	US-09-954-456-1583
2	40.8	2.1	2491	10	US-09-880-107-2391
3	39	2.0	2389	10	US-09-917-800A-1612
4	38	2.0	1386	10	US-09-925-301-562
5	37.6	1.9	1095	10	US-09-974-300-239
6	37.2	1.9	314	10	US-09-960-352-3971
7	36.6	1.9	1575	10	US-09-912-176-2
8	35.2	1.8	3276	10	US-09-925-302-242
9	34.8	1.8	1949	10	US-09-880-107-2388
10	34.8	1.8	3147	10	US-09-925-300-617
11	34.8	1.8	4024	12	US-10-044-090-86
12	34	1.8	2018	10	US-09-925-301-376
13	34	1.8	2068	10	US-09-880-107-1744
14	34	1.8	3370	12	US-10-044-090-339
15	33.8	1.8	401	10	US-09-795-668-1008
16	33.8	1.8	401	10	US-09-795-668-1008
17	33.8	1.8	586	10	US-09-349-015-3
18	33.8	1.8	1503841	10	US-09-795-668-1
19	33.8	1.8	1503841	10	US-09-795-668-1

20	33.6	1.7	3708	10	US-09-904-065-7	Sequence 7, Appli
c 21	33.4	1.7	413	10	US-09-728-446-947	Sequence 947, App
c 22	33.2	1.7	351	10	US-09-560-863-412	Sequence 412, App
c 23	33	1.7	3033	9	US-09-974-298-80	Sequence 80, Appl
c 24	33	1.7	3056	10	US-09-880-107-1765	Sequence 1765, Ap
c 25	32.8	1.7	443	9	US-10-046-935-1599	Sequence 1599, Ap
c 26	32.8	1.7	465	10	US-09-867-701-5341	Sequence 5341, Ap
c 27	32.8	1.7	2163	10	US-09-925-299-234	Sequence 234, App
c 28	32.8	1.7	2609	10	US-09-799-777-149	Sequence 149, App
c 29	32.8	1.7	3141	10	US-09-845-583-3	Sequence 3, Appli
c 30	32.4	1.7	1319	10	US-09-822-830A-383	Sequence 383, App
c 31	32.2	1.7	1557	10	US-09-962-290-7	Sequence 7, Appli
c 32	32.2	1.7	13029	10	US-09-815-242-4052	Sequence 4052, Ap
c 33	32	1.7	981	10	US-09-881-752A-283	Sequence 283, App
c 34	32	1.7	1140	10	US-09-861-289-15	Sequence 15, Appl
c 35	32	1.7	3708	10	US-09-904-065-5	Sequence 5, Appli
c 36	32	1.7	3708	10	US-09-904-065-9	Sequence 9, Appli
c 37	32	1.7	13613	10	US-09-861-289-3	Sequence 3, Appli
c 38	31.8	1.6	979	10	US-09-803-589-5	Sequence 5, Appli
c 39	31.8	1.6	1428	10	US-09-815-242-9802	Sequence 9802, Ap
c 40	31.4	1.6	2623	10	US-09-864-864-314	Sequence 314, App
c 41	31	1.6	420	10	US-09-864-761-10796	Sequence 10796, A
c 42	31	1.6	645	10	US-09-815-242-8018	Sequence 8018, Ap
c 43	31	1.6	1202	10	US-09-756-186-3	Sequence 3, Appli
c 44	30.8	1.6	442	10	US-09-764-878-392	Sequence 392, App
c 45	30.8	1.6	579	10	US-09-764-878-391	Sequence 391, App

ALIGNMENTS

RESULT 1  
US-09-954-456-1583  
; Sequence 1583, Application US/09954456  
; Patent No. US20020115057A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C  
; FILE REFERENCE: 689290-76  
; CURRENT APPLICATION NUMBER: US/09/954,456  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/60/233,617  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,052  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,923  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,134  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,637  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,638  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,711  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,720  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,840  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,863  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 2276  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1583  
; LENGTH: 2491  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-456-1583

Query Match 2.1%; Score 40.8; DB 10; Length 2491;  
Best Local Similarity 58.1%; Pred. No. 0.01; Mismatches 0; Gaps 0;  
Matches 72; Conservative 0; Indels 52



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; LENGTH: 314

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; PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 242  
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ORGANISM: Homo sapiens  
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NAME/KEY: misc feature  
LOCATION: (125)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (455)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (1014)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (3276)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-242

Query Match 1.8%; Score 35.2; DB 10; Length 3276;  
Best Local Similarity 52.8%; Pred. No. 0.81;  
Matches 76; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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Db 1306 TTTTTCAGTAAATTTTCAGAGCCCAAACTTTGTTTACACTATAGCTTAAGACAAACA 1247

QY 1133 GTGTGCGGTGCTCTCTCAGGT 1156

Db 1246 GGTGTGGGTATGTTCACTGTGGT 1223

## RESULT 9

US-09-880-107-2388

Sequence 2388, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

PRIOR FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2388

LENGTH: 1949

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020142981A1 M68840

Query Match 1.8%; Score 34.8; DB 10; Length 1949;  
Best Local Similarity 49.5%; Pred. No. 0.79;  
Matches 90; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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QY 1275 GGCGTCGGCTGTATAGTACGATCGGCTCGGGCGCGTGTCCGAAGCAAAAAGGTGGT 1334

Db 823 AAGTGACAACATCATCATAGAGAGCGCTGAACCATGAACATTATGATGCAATACGTAAT 882

QY 1335 GGTTCGTTACCGACAACATTTGATATCCACCTTGACATTTTTCACCACTCTTCCCGCCGA 1394

Db 883 TAATGCGATCCCTCCGACCTTGACTGCCAAGATTCACTTCAGACCAGAGCTTCCAGCAGA 942

QY 1395 GA 1396

Db 943 GA 944

## RESULT 10

US-09-925-300-617

Sequence 617, Application US/09925300

Patent No. US20020151681A1

GENERAL INFORMATION:

APPLICANT: Steve Ruben,

APPLICANT: Craig Rosen,

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: FA101

CURRENT APPLICATION NUMBER: US/09/925,300

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05988

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 617

LENGTH: 3147

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-300-617

Query Match 1.8%; Score 34.8; DB 10; Length 3147;  
Best Local Similarity 49.5%; Pred. No. 1.1;  
Matches 90; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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Db 303 AATGAGACCTCTCTCGGAGACCAAGTGAAGCTGAACCATCTGTCACTCAGTTGACCAGTC 362

QY 1275 GGCGTCGGCTGTATAGTACGATCGGCTCGGGCGCGTGTCCGAAGCAAAAAGGTGGT 1334

Db 363 AAGTGACAACATCATCATAGAGAGCGCTGAACCATGAACATTATGATGCAATACGTAAT 422

QY 1335 GGTTCGTTACCGACAACATTTGATATCCACCTTGACATTTTTCACCACTCTTCCCGCCGA 1394

Db 423 TAATGCGATCCCTCCGACCTTGACTGCCAAGATTCACTTCAGACCAGAGCTTCCAGCAGA 482

QY 1395 GA 1396

Db 483 GA 484

## RESULT 11

US-10-044-090-86

Sequence 86, Application US/10044090

Patent No. US20020137081A1

GENERAL INFORMATION:

APPLICANT: Olga Bandman

TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION

FILE REFERENCE: PA-0028 US

CURRENT APPLICATION NUMBER: US/10/044,090

PRIOR FILING DATE: 2002-01-09

NUMBER OF SEQ ID NOS: 850

SOFTWARE: PERL Program

SEQ ID NO 86

LENGTH: 4024

TYPE: DNA

ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1273213CB1
US-10-044-090-86

Query Match      1.8%; Score 34.8; DB 12; Length 4024;
Best Local Similarity 49.5%; Pred. No. 1.2;
Matches 90; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1215 AAAGAACTTGTTCAGGCTCAGTGACCTCAACACCCCGTGGTGAATTGAGCAGTC 1274
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 815 AATGACCTCCTCGGAGCAAGTGAAGCTGAACCATCTGTCTCACTCAGCTTGACCACTC 874
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1275 GCGTCGGCTGTATAGTACGATCGCTCGGCGCGGTTCCTCGAAGCAAAAAGTGCT 1334
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 875 AAGTGAACATCATGAGACGCTGAACCATGAACATATATGATGTCATATACGTAAT 934
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1335 GGTTCCTTACCACACATTTGATCCACCTTTGACATTTTACCACTCTTCCCGCGA 1394
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 935 TAATGCGATCCCTCGACCTTGACTGCCAAGATTCACTTCAGACCAGAGCTTCCAGCAGA 994
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1395 GA 1396
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Db 995 GA 996
      ||

RESULT 12
US-09-925-301-376
; Sequence 376, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 376
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1997)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2012)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-376

Query Match      1.8%; Score 34; DB 10; Length 2018;
Best Local Similarity 48.9%; Pred. No. 1.5;
Matches 91; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 119 AAGAGCTTTGGCGGTGACAGACCCAGCTACGAGAAACAGGTGCCCAAGCATTCGCCA 178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 836 AGGAGCTTTAGGTATTCAGCCGCTGCTCTTTCAACATGTCCAGCCAGCAGGTGCTG 895
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 179 ATCTGCGAGCTTGCTTGCCTGCTGAGTGGAGCTCTTCAACGACGCTCACCAGCTCAATT 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 896 CTGTTGGAATTCACCTCAGTGAAGTGAAGCCCAAGCTCTGATGATCTCTATA 955
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 239 ACTACATCTGCTACGACCCGCGAGCAAACTCACCAGCAATTCGAGATGGGTGAAGTCTA 298
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 956 AAACCTCACACCCATCTCAGCGGCATATGCAAGAGCAGAGGGGCTGATAGGATGCTT 1015
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 299 CCTTTG 304
      |||||
Db 1016 CATTTG 1021
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RESULT 14
US-10-044-090-339
; Sequence 339, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 339
; LENGTH: 3370
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 346535.6
US-10-044-090-339

Query Match      1.8%; Score 34; DB 12; Length 3370;
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	Best Local Similarity	50.0%; Pred. No. 2;	Mismatches	85; Indels	0; Gaps	0;
	Matches	85; Conservative	0;			
QY	379	GATGCCACGGCCTCGTGCCAGGACACTGCAGCCCCAGACAACGTTCGGACGCTGTGTAGT	438			
Db	1359	GGTGCCTGGCGTTGGGCCCGAGCGCTTGAGCGCTTCGCTCCCGGCGAGCTGCTG	1418			
QY	439	GTGGCGCTGGCTTGAGCGGTTTGAGAGCGCACCAAGTCCAGGCCCGCGCTGTCTC	498			
Db	1419	CTGGTCTGGGATGATCATCTTGCCTGTGGTGTGTGACAGTTGATCGCGGCCGCC	1478			
QY	499	TGCTCGTTCTTTGAGCGATGATCGTTAGGGGAAAGACTCTGACCGT	548			
Db	1479	AGCTGGACCCGGCGCTCGCGCGCTTCGGCGCCTGGCGGTGCTCT	1528			

RESULT 15

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RES001_13
US-09-795-668-1008
? Sequence 1008, Application US/09795668
? Patent NO. US20020045577A1
? GENERAL INFORMATION:
? APPLICANT: Stefansson, Hreinn
? APPLICANT: Steinhorsdottir, Valgerdur
? APPLICANT: Gulcher, Jeffrey R.
? TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
? FILE REFERENCE: 2345-2004-001
? CURRENT APPLICATION NUMBER: US/09/795,668
? CURRENT FILING DATE: 2001-02-28
? PRIOR APPLICATION NUMBER: US 09/515,716
? PRIOR FILING DATE: 2000-02-28
? NUMBER OF SEQ ID NOS: 1531
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1008
? LENGTH: 401
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-795-668-1008

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	Query Match	1.8%; Score 33.8; DB 10; Length 401;	
	Best Local Similarity 48.6%; Pred. No. 0.62;		
	Matches 89; Conservative 1; Mismatches 93; Indels 0; Gaps 0;		
Qy	1381	CCTCTCCCGCGAGAAGCAACGATTGGCGAAAAATCTACTCTCGGCTACTATACGAAG 1440	
		:	
Db	176	CTTCAACCTGCTGATGCTAGCACYACAGCAGCACCATTCAGGCCCACTACATTTT 235	
Qy	1441	ATAGTCTTCGTATGGACAACCCTGGTGCGCGAACAAGGCTTCTCGGCGCTCTCCAA 1500	
Db	236	AAATTTTTTTTAGAGACGATCTCTGC GCATGTTTCCCAAGCTGGCTTGAACCCCTGGCC 295	
Qy	1501	TCGAGCTGTGACCCCATCTCATTTCCGAGAGATACCGACATCGAAGTCGATCGGCAATGG 1560	
Db	296	TCANGCNTCTCCCACCTCAGCTTCCCTTAAGTACCAGGATTACAGGCATAGCCACTGA 355	
Qy	1561	TCC 1563	
Db	356	GCC 358	

Search completed: November 12, 2002, 05:34:51  
Job time : 160 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: November 12, 2002, 05:30:45 ; Search time 5080 seconds  
(without alignments)  
11051.046 Million cell updates/sec

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Perfect score: 1929  
Sequence: 1 atggcacttgaccagagcta.....gctctgtgcagcatag 1929

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

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					28:	em_un:*			
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					30:	em_htg_hum:*			
					31:	em_htg_inv:*			
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					33:	em_htg_mus:*			
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					38:	em_sy:*			
					39:	em_htgo_hum:*			
					40:	em_htgo_mus:*			
					41:	em_htgo_other:*			

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1929	100.0	1929	6	ARI45464	ARI45464 Sequence
2	1827	94.7	1929	6	ARI45465	ARI45465 Sequence
3	324	16.8	1389	6	ARI45447	ARI45447 Sequence
4	324	16.8	1389	6	ARI45474	ARI45474 Sequence
5	324	16.8	1392	6	ARI45449	ARI45449 Sequence
6	324	16.8	1392	6	ARI45476	ARI45476 Sequence
7	324	16.8	1442	6	ARI45448	ARI45448 Sequence
8	324	16.8	1442	6	ARI45475	ARI45475 Sequence
9	324	16.8	1464	6	ARI45456	ARI45456 Sequence
10	324	16.8	1464	6	ARI45483	ARI45483 Sequence
11	324	16.8	1673	6	ARI45454	ARI45454 Sequence
12	324	16.8	1673	6	ARI45481	ARI45481 Sequence
13	324	16.8	1803	6	ARI45457	ARI45457 Sequence
14	324	16.8	1803	6	ARI45484	ARI45484 Sequence
15	324	16.8	1930	6	ARI45466	ARI45466 Sequence
16	324	16.8	2079	6	ARI45455	ARI45455 Sequence
17	324	16.8	2079	6	ARI45482	ARI45482 Sequence
18	324	16.8	2490	6	ARI45462	ARI45462 Sequence
19	324	16.8	2490	6	ARI45489	ARI45489 Sequence
20	324	16.8	2976	6	ARI45459	ARI45459 Sequence
21	324	16.8	2976	6	ARI45486	ARI45486 Sequence
22	324	16.8	3003	6	ARI45458	ARI45458 Sequence
23	324	16.8	3003	6	ARI45485	ARI45485 Sequence
24	324	16.8	3591	6	ARI45461	ARI45461 Sequence
25	324	16.8	3591	6	ARI45488	ARI45488 Sequence
26	324	16.8	3618	6	ARI45460	ARI45460 Sequence
27	324	16.8	3618	6	ARI45487	ARI45487 Sequence
28	167	8.7	1928	6	ARI45467	ARI45467 Sequence
29	167	8.7	1928	6	ARI45468	ARI45468 Sequence
30	165	8.6	1928	6	ARI45469	ARI45469 Sequence
31	124	6.4	372	6	ARI45443	ARI45443 Sequence
32	124	6.4	372	6	ARI45470	ARI45470 Sequence
33	75	3.9	182	6	ARI45444	ARI45444 Sequence
34	75	3.9	182	6	ARI45471	ARI45471 Sequence
35	28	1.5	28	6	ARI45446	ARI45446 Sequence
36	28	1.5	28	6	ARI45453	ARI45453 Sequence
37	28	1.5	28	6	ARI45473	ARI45473 Sequence
38	28	1.5	28	6	ARI45480	ARI45480 Sequence
39	28	1.5	37	6	ARI45463	ARI45463 Sequence
40	23	1.2	34	6	ARI45450	ARI45450 Sequence
41	23	1.2	34	6	ARI45451	ARI45451 Sequence
42	23	1.2	34	6	ARI45477	ARI45477 Sequence
43	23	1.2	34	6	ARI45478	ARI45478 Sequence
44	23	1.2	67309	9	AL157932	Human DNA
45	21	1.1	137152	2	AF004564	Oryza sat

ALIGNMENTS

RESULT 1						
ARI45464						
LOCUS	ARI45464	1929 bp	DNA	linear	PAT 08-AUG-2001	
DEFINITION	Sequence 35 from patent US 6211434.					
ACCESSION	ARI45464					
VERSION	ARI45464.1	GI:15107331				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 1929)					
TITLE	Duvick,J.P., Gilliam,J.T. and Maddox,J.R.					
JOURNAL	Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use					
	Patent: US 6211434-A 35 03-APR-2001;					

FEATURES		Location/Qualifiers		1. 1929		409 t		532 g		537 c	
source		/organism="unknown"		0;		0;		0;		0;	
BASE COUNT		451 a		537 c		532 g		537 c		532 g	
ORIGIN		Query Match		100.0%; Score 1929; DB 6; Length 1929;		Best Local Similarity		100.0%; Pred. No. 0;		Matches 1929; Conservative	
		0; Mismatches		0; Indels		0; Gaps		0;		0;	
QY	1	ATGGCATTGACACGAGCTACATCAATCCCAACAGCTGCCTCCCAAGAGGGTATATCC	60								
Db	1	ATGGCACTTGCACCGAGCTACATCAATCCCAACAGCTGCCTCCCAAGAGGGTATATCC	60								
QY	61	CACATCGGGTAGGCCCAACAGAGGATATGACAATAGCTGGACAGATTGGACAA	120								
Db	61	CACATCGGGTAGGCCCAACAGAGGATATGACAATAGCTGGACAGATTGGACAA	120								
QY	121	GACGCTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT	180								
Db	121	GACGCTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT	180								
QY	181	CTGCGAGCTTGCTTGTCTGCACTTGGAGCTCTTCAACAGAGCTCACCAAGCTCAATTAC	240								
Db	181	CTGCGAGCTTGCTTGTCTGCACTTGGAGCTCTTCAACAGAGCTCACCAAGCTCAATTAC	240								
QY	241	TACATCTGCTGACTACGCCCGGAGCAACTACCGCAATTGGAGATGGGTGAAGTCTACCT	300								
Db	241	TACATCTGCTGACTACGCCCGGAGCAACTACCGCAATTGGAGATGGGTGAAGTCTACCT	300								
QY	301	TTTGCCCTTTGACAGGCTCCCTCTTGTGACGCTGGTGCCAGTACCAGGCTTGCCTTCACT	360								
Db	301	TTTGCCCTTTGACAGGCTCCCTCTTGTGACGCTGGTGCCAGTACCAGGCTTGCCTTCACT	360								
QY	361	GAATACCTTTGACGCTTATGCCAGCGGCTGTTGCCAGGACACTCGACCCACACAAAC	420								
Db	361	GAATACCTTTGACGCTTATGCCAGCGGCTGTTGCCAGGACACTCGACCCACACAAAC	420								
QY	421	GTTCGCGAGCTGTAGTGTGGCGGTGCTGCTTGAGCGGTTTGGAGACGCGACGCAAGTC	480								
Db	421	GTTCGCGAGCTGTAGTGTGGCGGTGCTGCTTGAGCGGTTTGGAGACGCGACGCAAGTC	480								
QY	481	CAGCGCGCGGCTGTCTTCTGCTGCTTCTTGAGCGGATGGATCGTGTAGGGGGAAGACT	540								
Db	481	CAGCGCGCGGCTGTCTTCTGCTGCTTCTTGAGCGGATGGATCGTGTAGGGGGAAGACT	540								
QY	541	CTGAGGTTACAATCGGGTCCCGCAGGAGCACTATCAACGACCTCGGCGCTCGTGGATC	600								
Db	541	CTGAGGTTACAATCGGGTCCCGCAGGAGCACTATCAACGACCTCGGCGCTCGTGGATC	600								
QY	601	AATGACAGCAACAAAGCAAGTATCCAGATTGTTGAAAGATTATTTGAGGGCGGAG	660								
Db	601	AATGACAGCAACAAAGCAAGTATCCAGATTGTTGAAAGATTATTTGAGGGCGGAG	660								
QY	661	CTCAGAGGACGCGGAATCAATCCATCAAGCAAGAGGATACACCACTACAGCT	720								
Db	661	CTCAGAGGACGCGGAATCAATCCATCAAGCAAGAGGATACACCACTACAGCT	720								
QY	721	CTTATGTTGACTCCCGGTAAAGCAATCCCACTTTGTGATGAGACCTCTCTGCGAGTGT	780								
Db	721	CTTATGTTGACTCCCGGTAAAGCAATCCCACTTTGTGATGAGACCTCTCTGCGAGTGT	780								
QY	781	AGAAATACAGTCACTGACTTCTGCTGCTGATCGAGGAGGATGGAAGTGCACCTTGC	840								
Db	781	AGAAATACAGTCACTGACTTCTGCTGCTGATCGAGGAGGATGGAAGTGCACCTTGC	840								
QY	841	GGAACTCTCCCGTATGTTCTGCTGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGC	900								
Db	841	GGAACTCTCCCGTATGTTCTGCTGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGC	900								
QY	901	GAGCCCTCAGGCGAGCGGCTGCACAGTGTGAGCTTTGCGCACTACTGTGAGAAGACCT	960								
Db	901	GAGCCCTCAGGCGAGCGGCTGCACAGTGTGAGCTTTGCGCACTACTGTGAGAAGACCT	960								

RESULT 2  
AR145465  
LOCUS

1929 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 37 from patent US 6211434.  
ACCESSION ARI45465  
VERSION ARI45465.1 GI:15107332  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1929)  
AUTHORS Duwick,J.P., Gilliam,J.T. and Maddox,J.R.  
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides  
and methods of use  
JOURNAL Patent: US 6211434-A 37 03-APR-2001;  
FEATURES Location/Qualifiers  
1..1929  
source /organism="unknown"  
BASE COUNT 451 a 539 c 532 g 407 t  
ORIGIN

Query Match 94.7%; Score 1827; DB 6; Length 1929;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1927; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACATTGACCGAGCTACATCAATCCCAACAGCTCGCTCCCGCAGCAGGGTATTCC 60  
DB 1 ATGGCACATTGACCGAGCTACATCAATCCCAACAGCTCGCTCCCGCAGCAGGGTATTCC 60

QY 61 CACATCGCGTAGGCCCCAAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120  
DB 61 CACATCGCGTAGGCCCCAAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120

QY 121 GACGCTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCAAGCATTCGCCAAT 180  
DB 121 GACGCTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCAAGCATTCGCCAAT 180

QY 181 CTGGAGCTTGCCCTTGCTGCAAGTTGGAGCCTCTTCAACAGCAGTCCACCAAGCTCAATTAC 240  
DB 181 CTGGAGCTTGCCCTTGCTGCAAGTTGGAGCCTCTTCAACAGCAGTCCACCAAGCTCAATTAC 240

QY 241 TACATCGTCACTACGCCCGCAGCAAACTCACCCCAATGGAGATGGGCTGAAGTCTACC 300  
DB 241 TACATCGTCACTACGCCCGCAGCAAACTCACCCCAATGGAGATGGGCTGAAGTCTACC 300

QY 301 TTTGCCCTTGACAGCTCCCTCTTGACAGCTGTGCGCAGTGTGCGCAGTACCGGCTTCACCT 360  
DB 301 TTTGCCCTTGACAGCTCCCTCTTGACAGCTGTGCGCAGTGTGCGCAGTACCGGCTTCACCT 360

QY 361 GAATACCTCTTTGAGGTTGATGCCACGCGCTGGTGCCAGGACACTCGACCCAGACAAC 420  
DB 361 GAATACCTCTTTGAGGTTGATGCCACGCGCTGGTGCCAGGACACTCGACCCAGACAAC 420

QY 421 GTTCGGACGTGTAGTGTGGGCGCTGGCTTGAGCGGTTTGAGAGCGGCACGCAAGTC 480  
DB 421 GTTCGGACGTGTAGTGTGGGCGCTGGCTTGAGCGGTTTGAGAGCGGCACGCAAGTC 480

QY 481 CAGCGCCGGCTGTCTGCTGCTGCTTTGAGCGATGATGCTGAGGGGAAAGACT 540  
DB 481 CAGCGCCGGCTGTCTGCTGCTGCTTTGAGCGATGATGCTGAGGGGAAAGACT 540

QY 541 CTGAGCTACAATCGGTTCCCGCAGGACGACTATCAACGACCTCGCGCTGCGTGGATC 600  
DB 541 CTGAGCTACAATCGGTTCCCGCAGGACGACTATCAACGACCTCGCGCTGCGTGGATC 600

QY 601 AATCAGACACCAACGGAAGTATCCAGATTGTTGAAAGATTTCAATTGGAGGCGGAG 660  
DB 601 AATCAGACACCAACGGAAGTATCCAGATTGTTGAAAGATTTCAATTGGAGGCGGAG 660

QY 661 CTCAGAGGACCGCGGAATTCATCCATCAAGCAACAGCGGTACACCTACAGCT 720  
DB 661 CTCAGAGGACCGCGGAATTCATCCATCAAGCAACAGCGGTACACCTACAGCT 720

QY 721 CCTTATGGTGACTCCCGGTAAAGCAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT 780  
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QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCACCTGC 840  
DB 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCACCTGC 840

QY 841 GGAACCTCCTCCCGTATGCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900  
DB 841 GGAACCTCCTCCCGTATGCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900

QY 901 GAGCCCTCAGCGAAGCGGCTGCACAGTGTGAGCTTTCGGCGCACTACTGTGAGAAGACCT 960  
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QY 961 AAACCTTGCCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGGA 1020  
DB 961 AAACCTTGCCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGGA 1020

QY 1021 AGCCACAGGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCCACCGTCTCAG 1080  
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QY 1081 TAATATTGCTCGGACAAGAAAGACGCGGCGAGTATATGCGATGCAAAACAGGTGCGTG 1140  
DB 1081 TAATATTGCTCGGACAAGAAAGACGCGGCGAGTATATGCGATGCAAAACAGGTGCGTG 1140

QY 1141 CGGTGCTCTCAGGTAGGGACTCGTTTCTTAGTGGTCAATTCAGAGTATGAGTGCATT 1200  
DB 1141 CGGTGCTCTCAGGTAGGGACTCGTTTCTTAGTGGTCAATTCAGAGTATGAGTGCATT 1200

QY 1201 TGCCATGCCATGTCAAAAGCAACTTTGTCAGGCTCAGTGCACCTCAACACCCCGTCCGT 1260  
DB 1201 TGCCATGCCATGTCAAAAGCAACTTTGTCAGGCTCAGTGCACCTCAACACCCCGTCCGT 1260

QY 1261 GGAATTGACAGTGGCGCTCGGCTGTATAGTACGATCGGCTCGGGCGCTGTTCCGA 1320  
DB 1261 GGAATTGACAGTGGCGCTCGGCTGTATAGTACGATCGGCTCGGGCGCTGTTCCGA 1320

QY 1321 AGCAAAAGGTGGTGGTTTGTACCGACAACATGTAATCCACCTTGACATTTTCACCA 1380  
DB 1321 AGCAAAAGGTGGTGGTTTGTACCGACAACATGTAATCCACCTTGACATTTTCACCA 1380

QY 1381 CTTCTTCCCGCAGAGAAGCAATTTGGCGGAAAATCTATCTCGGCTACTATAGCAAG 1440  
DB 1381 CTTCTTCCCGCAGAGAAGCAATTTGGCGGAAAATCTATCTCGGCTACTATAGCAAG 1440

QY 1441 ATAGTCTTCGTATGGACACCGCTGGTGGCGCGCAACAGGCTTCTCGGGCGCTCTCAA 1500  
DB 1441 ATAGTCTTCGTATGGACACCGCTGGTGGCGCGCAACAGGCTTCTCGGGCGCTCTCAA 1500

QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGATACAGCATCGAAGTCGATCGGCAATGG 1560  
DB 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGATACAGCATCGAAGTCGATCGGCAATGG 1560

QY 1561 TCCATTACCTGTTTCAATGGTCGAGACCGGAGCGGAGTGGTCCCAACAGTCCCAAGCAG 1620  
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QY 1801 CCGTTTCAAGTGTTCATTTCGTTGGAACGAGCGCTCTTTAGTTTGAAGAGGTATATG 1860  
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Qy 1921 GCAGCATAG 1929
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Db 1921 GCAGCATAG 1929

RESULT 3
AR145447
LOCUS AR145447 1389 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6211434.
ACCESSION AR145447
VERSION AR145447.1 GI:15107314
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1389)
AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 5 03-APR-2001;
FEATURES
source Location/Qualifiers
1..1389
/organism="unknown"
BASE COUNT 332 a 370 c 395 g 292 t
ORIGIN

Query Match 16.8%; Score 324; DB 6; Length 1389;
Best Local Similarity 99.7%; Pred. No. 4.6e-168;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1555 CAATGTCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTCCCAACAGTCC 1614
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Db 1075 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGACGCTACGAGAACGCCGG 1134

Qy 1675 GCCCAAGTCCCAGAGCCGCGCAACGTCCTCGAAATCGAGTGGTCCGAGCAGCAGTATTC 1734
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Qy 1735 CAAGGAGCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCAGTGGTTCGGCGCTC 1794
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Db 1255 AGAAGCGGTTCAAGTGTGTTCATTTCTGGGAACGAGACGCTTTTAGTTTGGAAAGG 1314

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Qy 1915 GTGCCAGCAGCATAG 1929
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RESULT 4
AR145474
LOCUS AR145474 1389 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6211435.
ACCESSION AR145474
VERSION AR145474.1 GI:15107341
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1389)
AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 10 03-APR-2001;
FEATURES
source Location/Qualifiers
1..1392
/organism="unknown"
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ORIGIN

Query Match 16.8%; Score 324; DB 6; Length 1392;
Best Local Similarity 99.7%; Pred. No. 4.6e-168;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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REFERENCE 1 (bases 1 to 1389)
AUTHORS Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211435-A 5 03-APR-2001;
FEATURES
source Location/Qualifiers
1..1389
/organism="unknown"
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RESULT 5
AR145449
LOCUS AR145449 1392 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 10 from patent US 6211434.
ACCESSION AR145449
VERSION AR145449.1 GI:15107316
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1392)
AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 10 03-APR-2001;
FEATURES
source Location/Qualifiers
1..1392
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BASE COUNT 335 a 370 c 395 g 292 t
ORIGIN

Query Match 16.8%; Score 324; DB 6; Length 1392;
Best Local Similarity 99.7%; Pred. No. 4.6e-168;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1555 CAATGTCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTCCCAACAGTCC 1614
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Db 1018 CAATGTCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTCCCAACAGTCC 1077
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JOURNAL	Patent: US 6211435-A 7 03-APR-2001;
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ORIGIN	/organism="unknown"
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Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
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Db	1308 AGNACCCGTTCAAGTGTGTTTCATTTCGTTGGAACGGAGAGCTCTTTAGTTTGGAAAGGG 1367
QY	1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTCGAGAAGTTGTGGCTAGCCTG 1914
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QY	1915 GTGCCAGCAGCATAG 1929
Db	1428 GTGCCAGCAGCATAG 1442
RESULT 9	
ARI45456	
LOCUS	ARI45456 1464 bp DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 20 from patent US 6211434.
ACCESSION	ARI45456
VERSION	ARI45456.1 GI:15107323
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1464)
AUTHORS	Duwick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE	Amino polyol amine oxidase polynucleotides and related polypeptides
JOURNAL	Patent: US 6211434-A 20 03-APR-2001;
FEATURES	Location/Qualifiers
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Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
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QY	1615 AAGCAGGTACGACAAAGTCTCTCTGCGGACCAACTCCGCGCAGGCTACGAGAACGCCGGG 1674
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QY	1675 GCCCAAGTCCCGAGCGGCCCAACGTGCTCGAAATCGAGTGGTGAAGCAGCAGTATTTC 1734
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QY	1735 CAAGAGTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTGCGCGCTC 1794
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QY	1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTCGAGAAGTTGTGGCTAGCCTG 1914
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Db	1450 GTGCCAGCAGCATAG 1464
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LOCUS	ARI45483 1464 bp DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 20 from patent US 6211435.
ACCESSION	ARI45483
VERSION	ARI45483.1 GI:15107350
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1464)
AUTHORS	Duwick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
TITLE	Amino polyol amine oxidase polynucleotides and related polypeptides
JOURNAL	Patent: US 6211435-A 20 03-APR-2001;
FEATURES	Location/Qualifiers
source	1. .1464
BASE COUNT	343 a 405 c 409 g 307 t
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Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
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QY	1615 AAGCAGGTACGACAAAGTCTCTCTGCGGACCAACTCCGCGCAGGCTACGAGAACGCCGGG 1674
Db	1150 AAGCAGGTACGACAAAGTCTCTCTGCGGACCAACTCCGCGCAGGCTACGAGAACGCCGGG 1209
QY	1675 GCCCAAGTCCCGAGCGGCCCAACGTGCTCGAAATCGAGTGGTGAAGCAGCAGTATTTC 1734
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Db	1450 GTGCCAGCAGCATAG 1464



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Qy 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTCTCTCAGAAAGTTGGCTAGCCTG 1914

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Qy 1915 GTGCCAGCAGCATAG 1929

Db 1789 GTGCCAGCAGCATAG 1803

RESULT 14

ARI145484

LOCUS ARI145484 1803 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 22 from patent US 6211435.

ACCESSION ARI145484

VERSION ARI145484.1 GI:15107351

KEYWORDS

SOURCE unknown.

ORGANISM unknown.

REFERENCE unclassified.

AUTHORS 1 (bases 1 to 1803)

TITLE Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.

JOURNAL Amino polyol amine oxidase polynucleotides and related polypeptides

FEATURES and methods of use

source Patent: US 6211435-A 22 03-APR-2001;

Location/Qualifiers

1. .1803

BASE COUNT 424 a 501 c 502 g 376 t

ORIGIN

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Best Local Similarity 99.7%; Pred. No. 4.5e-168;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1735 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1794

Db 1609 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1668

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Db 1789 GTGCCAGCAGCATAG 1803

RESULT 15

ARI145466

LOCUS ARI145466 1930 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 39 from patent US 6211434.

ACCESSION ARI145466

VERSION ARI145466.1 GI:15107333

KEYWORDS

SOURCE unknown.

ORGANISM unknown.

REFERENCE unclassified.

AUTHORS 1 (bases 1 to 1930)

TITLE Duvick,J.P., Gilliam,J.T. and Maddox,J.R.

JOURNAL Amino polyol amine oxidase polynucleotides and related polypeptides

FEATURES and methods of use

source Patent: US 6211434-A 39 03-APR-2001;

Location/Qualifiers

1. .1930

BASE COUNT 449 a 551 c 537 g 412 t 1 others

ORIGIN

Query Match 16.8%; Score 324; DB 6; Length 1930;

Best Local Similarity 99.7%; Pred. No. 4.5e-168;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1615 AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGACGCTACGAGAACGCGCGG 1674

Db 1616 AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGACGCTACGAGAACGCGCGG 1675

Qy 1675 GCCCAAGTCCAGAGCGCGCCACGCTCTGAAATCGAGTGGTCTGAAAGCAGCATATTTTC 1734

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Qy 1915 GTGCCAGCAGCATAG 1929

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	324	16.8	1392	AAZ58394	Amino polyol amine
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8	324	16.8	1442	AAZ58393	DNA encoding an am
9	324	16.8	1464	AAZ58401	DNA encoding amino

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12	324	16.8	1673	21	AAZ58395	DNA encoding an am
13	324	16.8	1803	21	AAZ58402	Exophiala spinifer
14	324	16.8	1803	21	AAZ60641	DNA encoding a ful
15	324	16.8	1930	21	AAZ58384	Exophiala spinifer
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17	324	16.8	2079	21	AAZ60639	DNA encoding an am
18	324	16.8	2490	21	AAZ58407	DNA encoding GST-t
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29	167	8.7	1928	21	AAZ58386	Rhinocladiaella atr
30	155	8.6	1928	21	AAZ58387	Rhinocladiaella atr
31	124	6.4	372	21	AAZ58388	Exophiala spinifer
32	124	6.4	372	21	AAZ60664	Nucleotide sequenc
33	75	3.9	182	21	AAZ58389	Exophiala spinifer
34	75	3.9	182	21	AAZ60663	Nucleotide sequenc
35	28	1.5	28	21	AAZ58391	Primer N21988 used
36	28	1.5	28	21	AAZ58399	Amino polyol amine
37	28	1.5	28	21	AAZ60629	5' RACE primer use
38	28	1.5	28	21	AAZ60637	PCR primer N21968
39	28	1.5	37	21	AAZ58408	Primer 23294 desig
40	23	1.2	34	21	AAZ58396	Primer N23256 desi
41	23	1.2	34	21	AAZ58397	Primer N23259 desi
42	23	1.2	34	21	AAZ60634	PCR primer N23256
43	23	1.2	34	21	AAZ60635	PCR primer N23259
44	20	1.0	5990	22	AAK67673	Human immune/haema
45	20	1.0	6118	23	ABL07290	Drosophila melanog

ALIGNMENTS

RESULT 1

AAZ58382

ID AAZ58382 standard; DNA; 1929 BP.

XX

AC AAZ58382;

XX

DT 23-MAY-2000 (first entry)

XX

DE Exophiala spinifera amino polyol amine oxidase ESP002\_C2 DNA.

XX

KW Amino polyol amine oxidase; fumonis; mycotoxin; transgenic plant;

KW detoxification; animal feed; silage; selectable marker; ds.

XX

OS Exophiala spinifera.

XX

FH Key Location/Qualifiers

FT CDS 1..1929

FT /tag= a

FT /note= "contains introns"

FT intron 739..811

FT /tag= b

FT intron 1134..1186

FT /tag= c

XX

XX WO200004159-A1.

PN

XX (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
XX  
PI DuVick JP, Gilliam JT, Maddox JR;  
XX  
DR WPI; 2000-182425/16.  
XX P-PSDB; AAY58900.  
XX  
XX New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading fumonisin or structurally related mycotoxin in processed  
PT grain or in silage  
XX  
PS Claim 1; Page 137-138; 154pp; English.  
XX  
XX The present sequence is that of an isolated nucleic acid,  
CC designated ESP002\_C2, of Exophiala spinifera isolate ESP002,  
CC which encodes an amino polyol amine oxidase (APAO, see AAY58900)  
CC capable of degrading fumonisin, its hydrolysis product AP1, and  
CC related mycotoxins. The DNA was obtained by PCR amplification of  
CC ESP002 mycelial DNA using primers based on APAO of E. spinifera  
CC ATCC 74269. The invention provides APAO polynucleotides (see  
CC AA258383-87) and polypeptides (see AAY58900-05) of E. spinifera and  
CC Rhinocladella atrovirens. The polynucleotides are used to transform  
CC plant cells normally susceptible to Fusarium or other toxin-producing  
CC fungus infection. Transgenic plants can be regenerated from the  
CC transformed plant cells. Also provided are methods for expressing  
CC both APAO and a fumonisin-esterase in a transgenic plant, and for  
CC producing APAO enzyme in prokaryotic and non-plant eukaryotic  
CC systems. Transgenic plants capable of degrading fumonisin or of  
CC producing the degrading enzymes are provided. Methods for  
CC detoxification of grain, grain processing, silage, food crops and  
CC in animal feed and rumen microorganisms are also disclosed. APAO  
CC polynucleotide is also useful as a selectable marker.  
XX  
SQ Sequence 1929 BP: 451 A; 537 G; 532 G; 409 T; 0 other;

Query Match 100.0%; Score 1929; DB 21; Length 1929;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCATTGACCGAGTACATCAATCCCCAACAGCTCGCTCCCGGAGGATATTC 60  
DB 1 ATGGCATTGACCGAGTACATCAATCCCCAACAGCTCGCTCCCGGAGGATATTC 60  
QY 61 CACATCGGCGTAGGGCCCAACGAGGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120  
DB 61 CACATCGGCGTAGGGCCCAACGAGGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120  
QY 121 GACGCTTTGGGCGTGACAGACCCAGCCTACGAGAACAGGTTGGCCCAAGCATTCGCCAAT 180  
DB 121 GACGCTTTGGGCGTGACAGACCCAGCCTACGAGAACAGGTTGGCCCAAGCATTCGCCAAT 180  
QY 181 CTGCGAGCTTGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 CTGCGAGCTTGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 241 TACATCGTGGACTACGCCCGGACCAACTCACCGCAATTTGGAGATGGGCTGAAGTCTACC 300  
DB 241 TACATCGTGGACTACGCCCGGACCAACTCACCGCAATTTGGAGATGGGCTGAAGTCTACC 300  
QY 301 TTTGCCCTTTGACAGGCTCCCTCCTTGACGCTGGTGCCAGTACCGGCCCTTGCGTTCACT 360  
DB 301 TTTGCCCTTTGACAGGCTCCCTCCTTGACGCTGGTGCCAGTACCGGCCCTTGCGTTCACT 360  
QY 361 GAATACCTTTGAGGTTGATCCAGCGGCTGGTGCCAGGACACTCGACCCGACACAC 420  
DB 361 GAATACCTTTGAGGTTGATCCAGCGGCTGGTGCCAGGACACTCGACCCGACACAC 420  
QY 421 GTTGGGAGCTGGTGTGTTGGGCGCTGGCTTGAGCGGTTTGGAGACGCGACGCAAGTC 480  
DB 421 GTTGGGAGCTGGTGTGTTGGGCGCTGGCTTGAGCGGTTTGGAGACGCGACGCAAGTC 480

QY 481 CAGGCGCGCGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
DB 481 CAGGCGCGCGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
QY 541 CTGAGCGTACAATCGGGTCCCGGACGAGACTATCAACGACCTCGGCGCTGGTGGATC 600  
DB 541 CTGAGCGTACAATCGGGTCCCGGACGAGACTATCAACGACCTCGGCGCTGGTGGATC 600  
QY 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGCGGAG 660  
DB 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGCGGAG 660  
QY 661 CTCAGAGGACGACCGGAATTCATTCATCAAGCAACGAGGTACAACTACTACAGCT 720  
DB 661 CTCAGAGGACGACCGGAATTCATTCATCAAGCAACGAGGTACAACTACTACAGCT 720  
QY 721 CCTTATGCTGACTCCCGGTAAGCAATCCCACTTTGTTGATGAGAGCTCTGTGCGAGTGT 780  
DB 721 CCTTATGCTGACTCCCGGTAAGCAATCCCACTTTGTTGATGAGAGCTCTGTGCGAGTGT 780  
QY 781 AGAATACAGTCACTGACTCCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCACCTTGC 840  
DB 781 AGAATACAGTCACTGACTCCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCACCTTGC 840  
QY 841 GGAACCTCTCCCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
DB 841 GGAACCTCTCCCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
QY 901 GAGCCCTCAGGCAAGCGGCTCGACAGTGTGAGCTTCGCGGCACTACTGTGAGAAGACCT 960  
DB 901 GAGCCCTCAGGCAAGCGGCTCGACAGTGTGAGCTTCGCGGCACTACTGTGAGAAGACCT 960  
QY 961 AAATCTGCT 1020  
DB 961 AAATCTGCT 1020  
QY 1021 AGCCACGAGATCAGCATGCTTTTTCACCGGCTGATATCGGATGCAAAACAGGTCGCTG 1080  
DB 1021 AGCCACGAGATCAGCATGCTTTTTCACCGGCTGATATCGGATGCAAAACAGGTCGCTG 1080  
QY 1081 TAATATTGCTCGGACAAGAGGCGGCGGCTGATATCGGATGCAAAACAGGTCGCTG 1140  
DB 1081 TAATATTGCTCGGACAAGAGGCGGCGGCTGATATCGGATGCAAAACAGGTCGCTG 1140  
QY 1141 CGGTGCTCTCAGGTAGGGGACTCGCTTTCTTAGTGGTCAATCCAGGTATGCGAGTTCGATT 1200  
DB 1141 CGGTGCTCTCAGGTAGGGGACTCGCTTTCTTAGTGGTCAATCCAGGTATGCGAGTTCGATT 1200  
QY 1201 TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACTCAACACCCCGCTCGCT 1260  
DB 1201 TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACTCAACACCCCGCTCGCT 1260  
QY 1261 GGAATTGAGCAGTCGGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA 1320  
DB 1261 GGAATTGAGCAGTCGGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA 1320  
QY 1321 AGCAAAAGGTGGTGGTTCGTTACCGCAACATTTGATCCCACTTGACATTTTCACCA 1380  
DB 1321 AGCAAAAGGTGGTGGTTCGTTACCGCAACATTTGATCCCACTTGACATTTTCACCA 1380  
QY 1381 CCTCTTCCCGGAGAGCAAGCATTTGGCGGAAATCTATCTCGGCTACTATAGCAAG 1440  
DB 1381 CCTCTTCCCGGAGAGCAAGCATTTGGCGGAAATCTATCTCGGCTACTATAGCAAG 1440  
QY 1441 ATAGCTTCGCTATGGGCAACCCGCTGGTGGCGGAAACAGGCTTCTCGGCGCTCTCCAA 1500  
DB 1441 ATAGCTTCGCTATGGGCAACCCGCTGGTGGCGGAAACAGGCTTCTCGGCGCTCTCCAA 1500  
QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGCATCGAAGTCGATCGCAATGG 1560  
DB 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGCATCGAAGTCGATCGCAATGG 1560  
QY 1561 TCCATTACCTGTTTTCATGGTCGGAGACCCGGGAGGAGTGGTCCCAACAGTCCAAAGCAG 1620

Db 1561 TCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGCAG 1620  
QY 1621 GTACGACAAAAGCTCTGTGGACCAACTCCGCGCAGCTACGAGAACGCCGGGGCCCAA 1680  
Db 1621 GTACGACAAAAGCTCTGTGGACCAACTCCGCGCAGCTACGAGAACGCCGGGGCCCAA 1680  
QY 1681 GTCCAGAGCGCGCCGACGCTGCTGAAATCGAGTGGTCTGAAAGCAGCAGTATTTCCAAAGGA 1740  
Db 1681 GTCCAGAGCGCGCCGACGCTGCTGAAATCGAGTGGTCTGAAAGCAGCAGTATTTCCAAAGGA 1740  
QY 1741 GTCGAGCGCGCTATGGCTGAACGATCTCATFACACACTGGGTGGCGCTCAGAACG 1800  
Db 1741 GTCGAGCGCGCTATGGCTGAACGATCTCATFACACACTGGGTGGCGCTCAGAACG 1800  
QY 1801 CGGTTCAAGTGTTCATTTGCTTGAACGAGAGCTCTTTAGTTTGAAGGCTATATG 1860  
Db 1801 CGGTTCAAGTGTTCATTTGCTTGAACGAGAGCTCTTTAGTTTGAAGGCTATATG 1860  
QY 1861 GAAGGGCCATACGATCGGGTCAAGAGGTGCTGCAGAAAGTGTGGCTAGCTGTGCGCA 1920  
Db 1861 GAAGGGCCATACGATCGGGTCAAGAGGTGCTGCAGAAAGTGTGGCTAGCTGTGCGCA 1920  
QY 1921 GCAGCATAG 1929  
Db 1921 GCAGCATAG 1929

RESULT 2  
AAZ58383  
ID AAZ58383 standard; DNA; 1929 BP.  
XX  
AC AAZ58383;  
DT 23-MAY-2000 (first entry)  
XX  
DE Exophiala spinifera amino polyol amine oxidase ESP002\_C3 DNA.  
KW Amino polyol amine oxidase; fumonisins; mycotoxin; transgenic plant;  
KW detoxification; animal feed; silage; selectable marker; ds.  
XX  
OS Exophiala spinifera.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1929  
FT FT /\*tag= a  
FT FT /note= "contains introns"  
FT intron 739..811  
FT FT /\*tag= b  
FT intron 1134..1186  
FT FT /\*tag= c  
XX  
PN WO200004159-A1.  
XX  
PD 27-JAN-2000.  
XX  
PF 08-JUL-1999; 99WO-US15454.  
XX  
PR 15-JUL-1998; 98US-0092936.  
PR 21-MAY-1999; 99US-0135391.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
XX  
PI Duvick JP, Gilliam JT, Maddox JR;  
XX  
XX WPI; 2000-182425/16.  
DR P-PSDB; AAY58901.  
XX  
PT New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading fumonisins or structurally related mycotoxin in processed  
PT grain or in silage  
XX

PS Claim 1; Page 139-140; 154pp; English.  
XX  
The present sequence is that of an isolated nucleic acid,  
CC designated ESP002\_C3, of Exophiala spinifera isolate ESP002,  
CC which encodes an amino polyol amine oxidase (APAO, see AAY58901)  
CC capable of degrading fumonisins, its hydrolysis product API, and  
CC related mycotoxins. The DNA was obtained by PCR amplification of  
CC ESP002 mycelial DNA using primers based on APAO of E. spinifera  
CC ATCC 74269. The invention provides APAO polynucleotides (see  
CC AAZ58383-87) and polypeptides (see AAY58900-05) of E. spinifera and  
CC Rhinocladia atrovirens. The polynucleotides are used to transform  
CC plant cells normally susceptible to Fusarium or other toxin-producing  
CC fungus infection. Transgenic plants can be regenerated from the  
CC transformed plant cells. Also provided are methods for expressing  
CC both APAO and a fumonisin-esterase in a transgenic plant, and for  
CC producing APAO enzyme in prokaryotic and non-plant eukaryotic  
CC systems. Transgenic plants capable of degrading fumonisins or of  
CC producing the degrading enzymes are provided. Methods for  
CC detoxification of grain, grain processing, silage, food crops and  
CC in animal feed and rumen microorganisms are also disclosed. APAO  
CC polynucleotide is also useful as a selectable marker.  
XX  
SQ Sequence 1929 BP; 451 A; 539 C; 532 G; 407 T; 0 other;  
Query Match 94.7%; Score 1827; DB 21; Length 1929;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1927; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGGCAGCTTCACCGAGCTACATCAATCCCCCAAGAGTGGCTCCCGCAGGAGTATTC 60  
Db 1 ATGGCAGCTTCACCGAGCTACATCAATCCCCCAAGAGTGGCTCCCGCAGGAGTATTC 60  
QY 61 CACATCGGCTAGGCGCCAAACGAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120  
Db 61 CACATCGGCTAGGCGCCAAACGAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120  
QY 121 GAGCCTTTGGGCGGTGACAGACCCAGGCTACGAGAAACAGGTTGCCCAAGCATTCGCAAT 180  
Db 121 GAGCCTTTGGGCGGTGACAGACCCAGGCTACGAGAAACAGGTTGCCCAAGCATTCGCAAT 180  
QY 181 CTGGGAGCTTGGCTTGTGCTGAGTTGGAGCCTCTTCAACGACGTACCAGCTCAATTAC 240  
Db 181 CTGGGAGCTTGGCTTGTGCTGAGTTGGAGCCTCTTCAACGACGTACCAGCTCAATTAC 240  
QY 241 TACATCGTCACTACGCGCCGAGCAAACTCACCGCAATTGGAGATGGCTGAAGTCTACC 300  
Db 241 TACATCGTCACTACGCGCCGAGCAAACTCACCGCAATTGGAGATGGCTGAAGTCTACC 300  
QY 301 TTGCGCCTTGACAGGCTCCCTCTTGCACGCTGGTGCCAGTACCGGCTTGGCTTCACCT 360  
Db 301 TTGCGCCTTGACAGGCTCCCTCTTGCACGCTGGTGCCAGTACCGGCTTGGCTTCACCT 360  
QY 361 GAATACCTCTTTGAGTTGATGCCACGGCGCTGGTGCCAGGACACTCGACCCAGACAAAC 420  
Db 361 GAATACCTCTTTGAGTTGATGCCACGGCGCTGGTGCCAGGACACTCGACCCAGACAAAC 420  
QY 421 GTTCCGACGCTGGTGTGAGTGGCGCTTGGAGCGGTTTGAGAGCGGCGCCAAAGTC 480  
Db 421 GTTCCGACGCTGGTGTGAGTGGCGCTTGGAGCGGTTTGAGAGCGGCGCCAAAGTC 480  
QY 481 CAGCGCCCGGCTCTGTCTCCCTCGCTTGTAGGCGGATGGATCGTGTAGGGGAAAGACT 540  
Db 481 CAGCGCCCGGCTCTGTCTCCCTCGCTTGTAGGCGGATGGATCGTGTAGGGGAAAGACT 540  
QY 541 CTGAGCGTACAATCGGCTCCCGGAGGACGACTATCAACGACCTCGCGCTGGATC 600  
Db 541 CTGAGCGTACAATCGGCTCCCGGAGGACGACTATCAACGACCTCGCGCTGGATC 600  
QY 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGCGGAG 660  
Db 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGCGGAG 660  
QY 661 CTCAGAGGACGCGCGGAAATTCATCCATCAAGCAAGACGGGTACACCACTACAGCT 720

Db 661 CTTCCAGAGCAGCCGGAATTCATCCATCAAGCACAGACGGTACAACCACTACAGCT 720  
QY 721 CTTATGGTGACTCCCGGTAAAGACAATCCACATTTGTGATGAGACCTCTGTGCAAGTGT 780  
Db 721 CTTATGGTGACTCCCGGTAAAGACAATCCACATTTGTGATGAGACCTCTGTGCAAGTGT 780  
QY 781 AGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGGTGCAAGTGCACTTGC 840  
Db 781 AGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGGTGCAAGTGCACTTGC 840  
QY 841 GGAATCTCTCCCGGTATGCTGCTAGCTGATGCAAGAGATATAGCCTTGAAGACCCCAAGGC 900  
Db 841 GGAATCTCTCCCGGTATGCTGCTAGCTGATGCAAGAGATATAGCCTTGAAGACCCCAAGGC 900  
QY 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGACCT 960  
Db 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGACCT 960  
QY 961 AAACCTTGCTGCTGTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGGA 1020  
Db 961 AAACCTTGCTGCTGTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGGA 1020  
QY 1021 AGCCACAGATCAGATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCTCAG 1080  
Db 1021 AGCCACAGATCAGATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCTCAG 1080  
QY 1081 TAATATTGCTCGGACAGAAAGCGGGCAGTATATGCGATGCAAAACAGTGCCTG 1140  
Db 1081 TAATATTGCTCGGACAGAAAGCGGGCAGTATATGCGATGCAAAACAGTGCCTG 1140  
QY 1141 CGGTGCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCAITCCAGGTATGCACTGCGATT 1200  
Db 1141 CGGTGCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCAITCCAGGTATGCACTGCGATT 1200  
QY 1201 TGCATGCCATGTCAAAGAACTTTCTCAGGCTCAGTGCACCTCAACCCCGCTGCT 1260  
Db 1201 TGCATGCCATGTCAAAGAACTTTCTCAGGCTCAGTGCACCTCAACCCCGCTGCT 1260  
QY 1261 GGAATTGAGCAGTGGCGCTCGGGCTGTAGTACGATCGGCTCGGGCGCGGTGTCGA 1320  
Db 1261 GGAATTGAGCAGTGGCGCTCGGGCTGTAGTACGATCGGCTCGGGCGCGGTGTCGA 1320  
QY 1321 AGCAAAAGGTGGTGGTTTCTGTTACCGACAACATTTGATCCACCTTGACATTTTCACCA 1380  
Db 1321 AGCAAAAGGTGGTGGTTTCTGTTACCGACAACATTTGATCCACCTTGACATTTTCACCA 1380  
QY 1381 CCTCTCCCGCGAGAACGACATTTGGGGAATAATCTATCCTCGGCTACTATAGCAAG 1440  
Db 1381 CCTCTCCCGCGAGAACGACATTTGGGGAATAATCTATCCTCGGCTACTATAGCAAG 1440  
QY 1441 ATAGTCTTGTATGGACAACCCGTTGGCGGCAACAGGCTTCTCGGGCTCTCCAA 1500  
Db 1441 ATAGTCTTGTATGGACAACCCGTTGGCGGCAACAGGCTTCTCGGGCTCTCCAA 1500  
QY 1501 TCGAGTGTGACCCCATCTCATTTGCCAGAGATACGACATCGAAGTGCATCGGCAATGG 1560  
Db 1501 TCGAGTGTGACCCCATCTCATTTGCCAGAGATACGACATCGAAGTGCATCGGCAATGG 1560  
QY 1561 TCATTACTGTTTCATGGTGGAGACCCGGAGGAGTGGTCCCAACAGTCCCAAGCAG 1620  
Db 1561 TCATTACTGTTTCATGGTGGAGACCCGGAGGAGTGGTCCCAACAGTCCCAAGCAG 1620  
QY 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGAGCTACGAGAAGCGGGGCCCAA 1680  
Db 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGAGCCTACGAGAAGCGGGGCCCAA 1680  
QY 1681 GTCCAGAGCCGGCCAACTGCTCGAAATCGAGTGGTGGAGAGCAGTATTTCCAAAGGA 1740  
Db 1681 GTCCAGAGCCGGCCAACTGCTCGAAATCGAGTGGTGGAGAGCAGTATTTCCAAAGGA 1740  
QY 1741 GCTCCGAGCGCGTCTATGGGCTGACCATCTCATCACATGGGTTCGGCGCTCAGAACG 1800  
Db 1741 GCTCCGAGCGCGTCTATGGGCTGACCATCTCATCACATGGGTTCGGCGCTCAGAACG 1800

Db 1741 GCTCCGAGCGCGTCTATGGGCTGAACGATCTCATCACATGGGTTTCGGCGCTCAGAACG 1800  
QY 1801 CCGTTCAAGTGTGTTCAATTTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGTTATAG 1860  
Db 1801 CCGTTCAAGTGTGTTCAATTTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGTTATAG 1860  
QY 1861 GAAGGGCCCATACCATCGGTCACAGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920  
Db 1861 GAAGGGCCCATACCATCGGTCACAGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920  
QY 1921 GCAGCATAG 1929  
Db 1921 GCAGCATAG 1929  
RESULT 3  
ID AAZ58392 standard; cDNA; 1389 BP.  
XX AAZ58392;  
AC AAZ58392;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Amino polyol amine oxidase truncated DNA k0n0-395\_6.5.  
XX  
KW Amino polyol amine oxidase; funonisin; mycotoxin; transgenic plant;  
XX  
OS Exophiala spinifera.  
XX  
PN WO200004159-A1.  
XX  
PD 27-JAN-2000.  
XX  
PF 08-JUL-1999; 99WO-US15454.  
XX  
PR 15-JUL-1998; 98US-0092936.  
PR 21-MAY-1999; 99US-0135391.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
XX  
PI Duvick JP, Gilliam JT, Maddox JR;  
XX  
DR WPI: 2000-182425/16.  
DR P-PSDB; AAY58906.  
XX  
PT New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading funonisin or structurally related mycotoxin in processed  
PT grain or in silage -  
XX  
PS Example 6; Page 74-76; 154pp; English.  
XX  
CC The present sequence is that of polynucleotide k0n0-395\_6.5, which  
CC encodes a truncated, but still functional, amino polyol amine oxidase  
CC (APAO, see AAY58906). The polynucleotide was obtained by 3' and 5'  
CC RACE PCR using k0n0-395\_5 (see AAZ58388), a partial APAO cDNA of  
CC Exophiala spinifera. APAO is capable of degrading funonisin, its  
CC hydrolysis product API and related mycotoxins. The invention  
CC provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see  
CC AAY58900-05) of E. spinifera and Rhinocladia atrovirens. The  
CC polynucleotides are used to transform plant cells normally  
CC susceptible to Fusarium or other toxin-producing fungus infection.  
CC Also provided are methods for expressing APAO in transgenic plants,  
CC prokaryotic and non-plant eukaryotic systems. Methods for  
CC detoxification of grain, grain processing, silage, food crops and  
CC in animal feed and rumen microorganisms are also disclosed. APAO  
CC polynucleotide can also be used as a selectable marker.  
XX  
SQ Sequence 1389 BP; 332 A; 370 C; 395 G; 292 T; 0 other;  
Query Match 16.8%; Score 324; DB 21; Length 1389;  
Best Local similarity 99.7%; Pred. No. 1.8e-158;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGAGAGTGTGTCACACAGTCC 1614  
|||||  
Db 1015 CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGAGAGTGTGTCACACAGTCC 1074  
|||||  
QY 1615 AAGCAGGTACGACAAAGTCTCTGTCGGACCAACTCCGCGAGCCTACGAGAACGCCGGG 1674  
|||||  
Db 1075 AAGCAGGTACGACAAAGTCTCTGTCGGACCAACTCCGCGAGCCTACGAGAACGCCGGG 1134  
|||||  
QY 1675 GCCCAGTCCAGAGCCGCGCAACGTCGTCGAAATCGAGTGTGTCGAAACGACGATATTC 1734  
|||||  
Db 1135 GCCCAGTCCAGAGCCGCGCAACGTCGTCGAAATCGAGTGTGTCGAAACGACGATATTC 1194  
|||||  
QY 1735 CAAGAGTCTCCAGAGCCGCGCTATCGGCTGAACGATCTCATCACACTCGGTTGCGCGCTC 1794  
|||||  
Db 1195 CAAGAGTCTCCAGAGCCGCGCTATCGGCTGAACGATCTCATCACACTCGGTTGCGCGCTC 1254  
|||||  
QY 1795 AGAAGCCGCTCAAGTGTTCATTTCTGTTGGAACGGAGACGTCCTTTAGTTTGGAAAGGG 1854  
|||||  
Db 1255 AGAAGCCGCTCAAGTGTTCATTTCTGTTGGAACGGAGACGTCCTTTAGTTTGGAAAGGG 1314  
|||||  
QY 1855 TATATGGAAGGGCCATAGTCGGTCAACGAGTGTGTCGAGAGTGTGTCGCTAGCCTG 1914  
|||||  
Db 1315 TATATGGAAGGGCCATAGTCGGTCAACGAGTGTGTCGAGAGTGTGTCGCTAGCCTG 1374  
|||||  
QY 1915 GTGCCAGCAGCATAG 1929  
|||||  
Db 1375 GTGCCAGCAGCATAG 1389  
|||||

RESULT 4  
AAZ60630  
ID AAZ60630 standard; DNA; 1389 BP.  
XX  
AC AAZ60630;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE DNA encoding an aminopolylol amine oxidase clone trAPO.  
XX  
KW Aminopolylol amine oxidase; APO; mycotoxin degradation; antimicrobial;  
KW plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.  
XX  
OS Exophiala spinifera.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1389  
FT /\*tag= a  
FT /product= "aminopolylol amine oxidase"

WO200004160-A1.  
XX  
PN 27-JAN-2000.  
XX  
PD 08-JUL-1999; 99WO-US15455.  
XX  
PF 15-JUL-1998; 98US-0092936.  
XX  
PR (PION-) PIONEER HI-BRED INT INC.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;  
XX  
XX WPI; 2000-182426/16.  
XX P-PSDB; AAY68843.  
XX  
PT New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to  
PT generate plants resistant to Fusarium -  
XX  
XX Example 6; Page 75-77; 145pp; English.  
XX  
XX The present sequence encodes an Exophiala spinifera aminopolylol amine

CC oxidase (APO). The enzyme has homology to the flavin containing amine  
CC oxidase family, that oxidise primary amine to an aldehyde or ketone,  
CC releasing ammonia and hydrogen peroxide. The APO enzyme degrades  
CC mycotoxins that promote fungal invasion of plants. Destruction of  
CC mycotoxins by APO generates, as a by-product, hydrogen peroxide which  
CC is itself an antimicrobial and stimulates the plants own defensive  
CC systems. The APO polynucleotides are used to generate plants  
CC (particularly maize) that are resistant to Fusarium or other fungi  
CC that produce mycotoxins and/or to degrade such mycotoxins (e.g. during  
CC ensiling); for recombinant production of APO polypeptides; as  
CC selection markers for plant transformation; and to isolate related  
CC sequences from other organisms. The APO polypeptides are used to  
CC degrade mycotoxins in plant materials, including expression in  
CC engineered bacteria and fungi, e.g. rumen microflora.  
XX  
SQ Sequence 1389 BP; 332 A; 370 C; 395 G; 292 T; 0 other;

Query Match 16.8%; Score 324; DB 21; Length 1389;  
Best Local Similarity 99.7%; Pred. No. 1.8e-158;  
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGAGAGTGTGTCACACAGTCC 1614  
|||||  
Db 1015 CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGAGAGTGTGTCACACAGTCC 1074  
|||||  
QY 1615 AAGCAGGTACGACAAAGTCTCTGTCGGACCAACTCCGCGAGCCTACGAGAACGCCGGG 1674  
|||||  
Db 1075 AAGCAGGTACGACAAAGTCTCTGTCGGACCAACTCCGCGAGCCTACGAGAACGCCGGG 1134  
|||||  
QY 1675 GCCCAGTCCAGAGCCGCGCAACGTCGTCGAAATCGAGTGTGTCGAAACGACGATATTC 1734  
|||||  
Db 1135 GCCCAGTCCAGAGCCGCGCAACGTCGTCGAAATCGAGTGTGTCGAAACGACGATATTC 1194  
|||||  
QY 1735 CAAGAGTCTCCAGAGCCGCGCTATCGGCTGAACGATCTCATCACACTCGGTTGCGCGCTC 1794  
|||||  
Db 1195 CAAGAGTCTCCAGAGCCGCGCTATCGGCTGAACGATCTCATCACACTCGGTTGCGCGCTC 1254  
|||||  
QY 1795 AGAAGCCGCTCAAGTGTTCATTTCTGTTGGAACGGAGACGTCCTTTAGTTTGGAAAGGG 1854  
|||||  
Db 1255 AGAAGCCGCTCAAGTGTTCATTTCTGTTGGAACGGAGACGTCCTTTAGTTTGGAAAGGG 1314  
|||||  
QY 1855 TATATGGAAGGGCCATAGTCGGTCAACGAGTGTGTCGAGAGTGTGTCGCTAGCCTG 1914  
|||||  
Db 1315 TATATGGAAGGGCCATAGTCGGTCAACGAGTGTGTCGAGAGTGTGTCGCTAGCCTG 1374  
|||||  
QY 1915 GTGCCAGCAGCATAG 1929  
|||||  
Db 1375 GTGCCAGCAGCATAG 1389  
|||||

RESULT 5  
AAZ58394  
ID AAZ58394 standard; cDNA; 1392 BP.  
XX  
AC AAZ58394;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Amino polyol amine oxidase DNA clone K:trAPO.  
XX  
KW Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;  
KW detoxification; animal feed; silage; selectable marker; mutant; ss.  
XX  
OS Exophiala spinifera.  
OS Synthetic.  
XX  
PN WO200004159-A1.  
XX  
PD 27-JAN-2000.  
XX  
PF 08-JUL-1999; 99WO-US15454.  
XX  
PR 15-JUL-1998; 98US-0092936.

```
PR 21-MAY-1999; 99US-0135391.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
PI Duvick JP, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182425/16.
DR P-PSDB; AAY58909.
XX
XX New isolated polynucleotides, polypeptides useful for detecting and
PT degrading fumonisin or structurally related mycotoxin in processed
PT grain or in silage -
XX
XX Example 7; Page 81-83; 154pp; English.
XX
XX The present sequence is that of a polynucleotide encoded a truncated,
CC but still functional, amino polyol amine oxidase (K:trAPAO, see
CC AAY58909) of Exophiala spinifera. The polynucleotide was derived from
CC clone k0n0-395.6.5 (see AAY58392) to which was added a 5' lysine codon
CC (nucleotides 1-3), since many amine oxidases have a positively charged
CC amino acid near the N-terminus and upstream of a dinucleotide binding
CC site. The construct allowed heterologous expression of trAPAO in
CC Pichia pastoris and maize. The invention provides APAO polynucleotides
CC (see AAY58383-87) and polypeptides (see AAY58900-05) of E. spinifera and
CC Rhinocladia atrovirens. The polynucleotides are used to transform
CC plant cells normally susceptible to Fusarium or other toxin-producing
CC fungus infection. Also provided are methods for expressing APAO in
CC transgenic plants, prokaryotic and non-plant eukaryotic systems.
CC Methods for detoxification of grain, grain processing, silage, food
CC crops and in animal feed and rumen microorganisms are also disclosed.
CC APAO polynucleotide can also be used as a selectable marker.
XX
XX Sequence 1392 BP; 335 A; 370 C; 395 G; 292 T; 0 other;
SQ
Query Match 16.8%; Score 324; DB 21; Length 1392;
Best Local Similarity 99.7%; Pred. No. 1.8e-158;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1555 CAATGGTCCATTACCTGTTTCATGTGCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
DB 1018 CAATGGTCCATTACCTGTTTCATGTGCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1077
QY 1615 AAGCAGGTACGACAAAAGTCTCTGTGGGACCAACTCCGCGCAGCCTACGAGAACCCCGGG 1674
DB 1078 AAGCAGGTACGACAAAAGTCTCTGTGGGACCAACTCCGCGCAGCCTACGAGAACCCCGGG 1137
QY 1675 GCCAAGTCCAGAGCGCGCCACGTCGTCTGAAATCGAGTGTCTGCAAGCAGCAGTATTTC 1734
DB 1138 GCCAAGTCCAGAGCGCGCCACGTCGTCTGAAATCGAGTGTCTGCAAGCAGCAGTATTTC 1197
QY 1735 CAAGGAGCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGTTCGGCGCTC 1794
DB 1198 CAAGGAGCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGTTCGGCGCTC 1257
QY 1795 AGAACGCCGTTCAAGTGTGTTTCATTTTCGTTTGAACGGAGACGCTCTTTAGTTTGAAGGG 1854
DB 1258 AGAACGCCGTTCAAGTGTGTTTCATTTTCGTTTGAACGGAGACGCTCTTTAGTTTGAAGGG 1317
QY 1855 TATATGAAGGGCCATACGATCGGGTCAACGAGTGTCTGCAGAGATTGTGCTAGCCTG 1914
DB 1318 TATATGAAGGGCCATACGATCGGGTCAACGAGTGTCTGCAGAGATTGTGCTAGCCTG 1377
QY 1915 GTGCCAGCAGCATAG 1929
DB 1378 GTGCCAGCAGCATAG 1392
RESULT 6
ID AA260633
XX AA260633 standard; DNA; 1392 BP.
AC AA260633;
```

```
XX 16-MAY-2000 (first entry)
XX DNA encoding an aminopolylol amine oxidase clone K:trAPAO.
XX
XX Aminopolylol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
XX plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
XX
XX Synthetic.
XX Exophiala spinifera.
XX
XX Key Location/Qualifiers
XX CDS 1..1392
XX FT /*tag= a
XX FT /product= "aminopolylol amine oxidase"
XX FT /note= "the amino terminal Lys was added to the
XX FT protein sequence for optimized expression"
XX
XX WC200004160-Al.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15455.
XX
XX 15-JUL-1998; 98US-0092936.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182426/16.
DR P-PSDB; AAY68845.
XX
XX New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to
PT generate plants resistant to Fusarium -
XX
XX Example 7; Page 82-84; 145pp; English.
XX
XX The present sequence encodes an Exophiala spinifera aminopolylol amine
CC oxidase (APAO). The enzyme has homology to the flavin containing amine
CC oxidase family, that oxidise primary amine to an aldehyde or ketone,
CC releasing ammonia and hydrogen peroxide. The APAO enzyme degrades
CC mycotoxins that promote fungal invasion of plants. Destruction of
CC mycotoxins by APAO generates, as a by-product, hydrogen peroxide which
CC is itself an antimicrobial and stimulates the plants own defensive
CC systems. The APAO polynucleotides are used to generate plants
CC (particularly maize) that are resistant to Fusarium or other fungi
CC that produce mycotoxins and/or to degrade such mycotoxins (e.g. during
CC ensiling); for recombinant production of APAO polypeptides; as
CC selection markers for plant transformation; and to isolate related
CC sequences from other organisms. The APAO polypeptides are used to
CC degrade mycotoxins in plant materials, including expression in
CC engineered bacteria and fungi, e.g. rumen microflora.
XX
XX Sequence 1392 BP; 335 A; 370 C; 395 G; 292 T; 0 other;
SQ
Query Match 16.8%; Score 324; DB 21; Length 1392;
Best Local Similarity 99.7%; Pred. No. 1.8e-158;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1555 CAATGGTCCATTACCTGTTTCATGTGCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
DB 1018 CAATGGTCCATTACCTGTTTCATGTGCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1077
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACCCCGGG 1674
DB 1078 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACCCCGGG 1137
QY 1675 GCCCAAGTCCAGAGCGCGCCACGTCGTCTGAAATCGAGTGTCTGCAAGCAGCAGTATTTC 1734
DB 1138 GCCCAAGTCCAGAGCGCGCCACGTCGTCTGAAATCGAGTGTCTGCAAGCAGCAGTATTTC 1197
```

QY 1735 CAAGGAGCTCCGAGCGCGCTATGGCTGAACGATCTCATCACACTGGGTTCCGCGCTC 1794  
|||||  
Db 1198 CAAGGAGCTCCGAGCGCGCTATGGCTGAACGATCTCATCACACTGGGTTCCGCGCTC 1257  
|||||  
QY 1795 AGAAGCCGTTCAAGTGTTTCATTTCCTTGGACGGAGAGCTCTTTAGTTTGGAAAGGG 1854  
|||||  
Db 1258 AGAAGCCGTTCAAGAGTGTTTCATTTCCTTGGACGGAGAGCTCTTTAGTTTGGAAAGGG 1317  
|||||  
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGCTGCAGAAAGTTGTGGCTAGCCTG 1914  
|||||  
Db 1318 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGCTGCAGAAAGTTGTGGCTAGCCTG 1377  
|||||  
QY 1915 GTGCCAGCAGCATAG 1929  
|||||  
Db 1378 GTGCCAGCAGCATAG 1392  
|||||  
RESULT 7  
AAZ58393  
ID AAZ58393 standard; cDNA; 1442 BP.  
XX  
AC AAZ58393;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Amino polyol amine oxidase truncated DNA k0n0-395\_5.4.  
XX  
KW Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;  
KW detoxification; animal feed; silage; selectable marker; ss.  
XX  
OS Exophiala spinifera.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1442  
FT /\*tag= a  
FT /note= "contains an intron"  
FT intron 647..699  
FT /\*tag= b  
XX  
PN WO200004159-A1.  
XX  
PD 27-JAN-2000.  
XX  
PF 08-JUL-1999; 99WO-US15454.  
XX  
PR 15-JUL-1998; 98US-0092936.  
PR 21-MAY-1999; 99US-0135391.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
PA (CURA-) CURAGEN CORP.  
PI Duvick JP, Gilliam JT, Maddox JR;  
XX  
DR WPI; 2000-182425/16.  
DR P-PSDB; AAY58907, AAY58908.  
XX  
PT New isolated polynucleotides, polypeptides useful for detecting and  
PT degrading fumonisin or structurally related mycotoxin in processed  
PT grain or in silage -  
XX  
PS Example 6; Page 77-79; 154pp; English.  
XX  
CC The present sequence is that of polynucleotide k0n0-395\_5.4, which  
CC encodes a truncated, but still functional, amino polyol amine oxidase  
CC (trPAO-I, see AAY58907 and AAY58908). The polynucleotide was obtained  
CC by 3' and 5' RACE PCR using k0n0-395.5 (see AAZ58388), a partial APAO  
CC cDNA of Exophiala spinifera. APAO is capable of degrading fumonisin,  
CC its hydrolysis product Ap1 and related mycotoxins. The invention  
CC provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see  
CC AAY58900-05) of E. spinifera and Rhinocladiella atrovirens. The  
CC polynucleotides are used to transform plant cells normally  
CC susceptible to Fusarium or other toxin-producing fungus infection.  
CC Also provided are methods for expressing APAO in transgenic plants,

CC prokaryotic and non-plant eukaryotic systems. Methods for  
CC detoxification of grain, grain processing, silage, food crops and in  
CC animal feed and rumen microorganisms are also disclosed. APAO  
CC polynucleotide can also be used as a selectable marker.  
XX  
SQ Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;  
Query Match 16.8%; Score 324; DB 21; Length 1442;  
Best Local Similarity 99.7%; Pred. No. 1.8e-158;  
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1555 CAATGGTCCATTACCTGTTTCATGTGCGGAGACCGGGACGGAAGTGTCCCAACAGTCC 1614  
|||||  
Db 1068 CAATGGTCCATTACCTGTTTCATGTGCGGAGACCGGGACGGAAGTGTCCCAACAGTCC 1127  
|||||  
QY 1615 AAGCAGTAGCAGACAAAAGTCTGTCTGGGACCACCTCCGGGACCCCTACGAGAACGCCGG 1674  
|||||  
Db 1128 AAGCAGTAGCAGACAAAAGTCTGTCTGGGACCACCTCCGGGACCCCTACGAGAACGCCGG 1187  
|||||  
QY 1675 GCCCAAGTCCAGAGCGCGCAACGTGCTCGAAATCGAGTGTGCGAAGCAGCAGTATTC 1734  
|||||  
Db 1188 GCCCAAGTCCAGAGCGCGCAACGTGCTCGAAATCGAGTGTGCGAAGCAGCAGTATTC 1247  
|||||  
QY 1735 CAAGGAGCTCCGAGCGCGCTCTATGGCTGAACGATCTCATCACACTGGGTTCCGCGCTC 1794  
|||||  
Db 1248 CAAGGAGCTCCGAGCGCGCTCTATGGCTGAACGATCTCATCACACTGGGTTCCGCGCTC 1307  
|||||  
QY 1795 AGAAGCCGTTCAAGTGTTTCATTTCCTTGGACGGAGAGCTCTTTAGTTTGGAAAGGG 1854  
|||||  
Db 1308 AGAAGCCGTTCAAGAGTGTTTCATTTCCTTGGACGGAGAGCTCTTTAGTTTGGAAAGGG 1367  
|||||  
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGCTGCAGAAAGTTGTGGCTAGCCTG 1914  
|||||  
Db 1368 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGCTGCAGAAAGTTGTGGCTAGCCTG 1427  
|||||  
QY 1915 GTGCCAGCAGCATAG 1929  
|||||  
Db 1428 GTGCCAGCAGCATAG 1442  
|||||  
RESULT 8  
AAZ60631  
ID AAZ60631 standard; DNA; 1442 BP.  
XX  
AC AAZ60631;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE DNA encoding an aminopolyol amine oxidase clone trPAO-I.  
XX  
KW Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;  
KW plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.  
XX  
OS Exophiala spinifera.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1442  
FT /\*tag= a  
FT /product= "aminopolyol amine oxidase"  
FT /note= "contains an intron"  
FT exon 1..646  
FT /\*tag= b  
FT /number= 1  
FT intron 647..699  
FT /\*tag= c  
FT /number= 1  
FT exon 700..1439  
FT /\*tag= d  
FT /number= 2  
XX  
PN WO200004160-A1.  
XX  
PD 27-JAN-2000.

```
XX 08-JUL-1999; 99WO-US15455.
XX 15-JUL-1998; 98US-0092936.
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX Crasta OR, Duivick J, Folkerts O, Gilliam JT, Maddox JR;
XX WPI: 2000-182426/16.
XX P-PSDB; AAY68844.
XX New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to
XX generate plants resistant to Fusarium -
XX Example 6; Page 78-80; 145pp; English.
XX The present sequence encodes an Exophiala spinifera aminopolylol amine
XX oxidase (APAO). The enzyme has homology to the flavin containing amine
XX oxidase family, that oxidise primary amine to an aldehyde or ketone,
XX releasing ammonia and hydrogen peroxide. The APAO enzyme degrades
XX mycotoxins that promote fungal invasion of plants. Destruction of
XX mycotoxins by APAO generates, as a by-product, hydrogen peroxide which
XX is itself an antimicrobial and stimulates the plants own defensive
XX systems. The APAO polynucleotides are used to generate plants
XX (particularly maize) that are resistant to Fusarium or other fungi
XX that produce mycotoxins and/or to degrade such mycotoxins (e.g. during
XX ensilaging); for recombinant production of APAO polypeptides; as
XX selection markers for plant transformation; and to isolate related
XX sequences from other organisms. The APAO polypeptides are used to
XX degrade mycotoxins in plant materials, including expression in
XX engineered bacteria and fungi, e.g. rumen microflora.
XX Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
XX
XX Query Match 16.8%; Score 324; DB 21; Length 1442;
XX Best Local Similarity 99.7%; Pred. No. 1.8e-158;
XX Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1555 CAATGGTCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTCCCAACAGTCC 1614
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1068 CAATGGTCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTCCCAACAGTCC 1127
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1615 AAGCAGGTACGACAAAGTCTCTCTGGACCAACTCCCGCGAGCCCTACGAGAAGCGCCGG 1674
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1128 AAGCAGGTACGACAAAGTCTCTCTGGACCAACTCCCGCGAGCCCTACGAGAAGCGCCGG 1187
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1675 GCCCAAGTCCGAGACCGCGCCCAACGTGTCGAAATCGAGTGTGGAACGAGTATTTTC 1734
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1188 GCCCAAGTCCGAGACCGCGCCCAACGTGTCGAAATCGAGTGTGGAACGAGTATTTTC 1247
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1735 CAAGGAGTCTCCGAGCGCGCTCTATGGCTGAACGATCTCATCACACTGGGTTCGCGGCTC 1794
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1248 CAAGGAGTCTCCGAGCGCGCTCTATGGCTGAACGATCTCATCACACTGGGTTCGCGGCTC 1307
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1795 AGAAGCGGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGGG 1854
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1308 AGAAGCGGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGGG 1367
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1855 TATATGGAAGGGCCATACGATCGGCTCAACGAGGTGCTGAGAGTTGGCTAGGCTG 1914
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1368 TATATGGAAGGGCCATACGATCGGCTCAACGAGGTGCTGAGAGTTGGCTAGGCTG 1427
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1915 GTGCCAGCAGCATAG 1929
Db ||||||||||||||||||
QY 1428 GTGCCAGCAGCATAG 1442
Db ||||||||||||||||||
XX
RESULT 9
AAZ58401
ID AAZ58401 standard; cDNA: 1464 BP.
XX
```

```
AC AAZ58401;
XX 23-MAY-2000 (first entry)
XX DNA encoding amino polyol amine oxidase for expression in maize.
XX Amino polyol amine oxidase; APAO; fumonisin; mycotoxin;
XX transgenic plant; detoxification; animal feed; silage;
XX selectable marker; barley; alpha-amylase; signal peptide; maize;
XX ss.
XX Chimeric - Hordeum vulgare.
XX Chimeric - Exophiala spinifera.
XX Key Location/Qualifiers
XX sig_peptide 1..72 /*tag= a
XX mat_peptide 73..1461 /*product= "barley alpha-amylase signal peptide"
XX /*tag= b
XX misc_feature 73..75 /*product= "K:trAPAO"
XX /*tag= c
XX /*note= "extra lysine codon"
XX WO200004159-A1.
XX 27-JAN-2000.
XX 08-JUL-1999; 99WO-US15454.
XX 15-JUL-1998; 98US-0092936.
XX 21-MAY-1999; 99US-0135391.
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX Duivick JP, Gilliam JT, Maddox JR;
XX WPI: 2000-182425/16.
XX P-PSDB; AAY58912.
XX New isolated polynucleotides, polypeptides useful for detecting and
XX degrading fumonisin or structurally related mycotoxin in processed
XX grain or in silage -
XX Example 11; Page 94-96; 154pp; English.
XX
XX The present sequence is that of a polynucleotide encoding a
XX fusion protein (see AAY58912) composed of the barley alpha-amylase
XX signal peptide and K:trAPAO (see AAY58909), a truncated, but
XX functional, amino polyol amine oxidase of Exophiala spinifera.
XX The construct was designed for expression and secretion of
XX K:trAPAO in maize. Transgenic maize callus was produced. K:trAPAO
XX is capable of degrading fumonisin and related mycotoxins. The
XX invention provides APAO polynucleotides (see AAZ58383-87) and
XX polypeptides (see AAY58900-05) of E. spinifera and Rhinocladiella
XX atrovirens. The polynucleotides are used to transform plant cells
XX normally susceptible to Fusarium or other toxin-producing fungus
XX infection. Also provided are methods for expressing APAO in
XX transgenic plants, prokaryotic and non-plant eukaryotic systems.
XX Methods for detoxification of grain, grain processing, silage, food
XX crops and in animal feed and rumen microorganisms are also disclosed.
XX APAO polynucleotide can also be used as a selectable marker.
XX
XX Sequence 1464 BP; 343 A; 405 C; 409 G; 307 T; 0 other;
XX
XX Query Match 16.8%; Score 324; DB 21; Length 1464;
XX Best Local Similarity 99.7%; Pred. No. 1.8e-158;
XX Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1555 CAATGGTCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTCCCAACAGTCC 1614
|||
```



```
Db 1090 CAATGTCACATTACCTGTTTCATGTCGAGACCCGCGGAGCGAAGTGGTCCCAACAGTCC 1149
QY 1615 AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
PS |||||||
PS |||||||
Db 1150 AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1209
QY 1675 GCCAAGTCCAGAGCGCGGCGAAGTGTCTGAAATCGAGTGTCTGAAAGCAGCAGTATTTTC 1734
Db 1210 GCCAAGTCCAGAGCGCGGCGAAGTGTCTGAAATCGAGTGTCTGAAAGCAGCAGTATTTTC 1269
QY 1735 CAAGGAGTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1794
Db 1270 CAAGGAGTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1329
QY 1795 AGAACGCCGTTCAAGTGTGTCTATTCTTCTGGTGGAGCAGCAGTCTTTAGTTTGGAAAGG 1854
Db 1330 AGAACGCCGTTCAAGTGTGTCTATTCTTCTGGTGGAGCAGCAGTCTTTAGTTTGGAAAGG 1389
QY 1855 TATATGGAAGGGCCATACATCGGTCAACGAGGTGCTGCAGAACTTGTGGCTAGCCCTG 1914
Db 1390 TATATGGAAGGGCCATACATCGGTCAACGAGGTGCTGCAGAACTTGTGGCTAGCCCTG 1449
QY 1915 GTGCCAGCAGCATAG 1929
Db 1450 GTGCCAGCAGCATAG 1464

RESULT 10
AAZ60640
ID AAZ60640 standard; DNA; 1464 BP.
XX
AC AAZ60640;
XX
XX
DT 16-MAY-2000 (first entry)
XX
DE DNA encoding an aminopolylol amine oxidase for expression in maize.
XX
KW Aminopolylol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
KW plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
XX
OS Hordeum vulgare.
OS Synthetic.
OS Exophiala spinifera.
XX
FH Key Location/Qualifiers
FT CDS 1..1464
FT FT /*tag= a
FT FT /product= "aminopolylol amine oxidase"
FT FT 1..72
FT FT /*tag= b
FT FT /note= "barley alpha amylase signal sequence"
FT FT 73..1461
FT FT /*tag= c
FT FT /note= "aminopolylol amine oxidase, with an extra
FT FT amino terminal Lys residue for optimized
FT FT expression"
XX
PN WO200004160-AL.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15455.
XX
XX 15-JUL-1998; 98US-0092936.
XX
XX {PION-} PIONEER HI-BRED INT INC.
XX {CURA-} CURAGEN CORP.
XX
XX Crasta OR, Duwick J, Folkerts O, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182426/16.
XX P-PSDB; AAY68848.
XX
```

```
PT New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to
PT generate plants resistant to Fusarium -
XX
PS Example 11; Page 95-97; 145pp; English.
XX
CC The present sequence encodes an Exophiala spinifera aminopolylol
CC amine oxidase (APAO). The APAO enzyme has homology to the flavin
CC containing amine oxidase family, that oxidise primary amine to an
CC aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO
CC enzyme degrades mycotoxins that promote fungal invasion of plants.
CC destruction of mycotoxins by APAO generates, as a by-product, hydrogen
CC peroxide which is itself an antimicrobial and stimulates the plants
CC own defensive systems. The APAO polynucleotides are used to generate
CC plants (particularly maize) that are resistant to Fusarium or other fungi
CC that produce mycotoxins and/or to degrade such mycotoxins (e.g. during
CC ensiling); for recombinant production of APAO polypeptides; as
CC selection markers for plant transformation; and to isolate related
CC sequences from other organisms. The APAO polypeptides are used to
CC degrade mycotoxins in plant materials, including expression in
CC engineered bacteria and fungi, e.g. rumen microflora.
XX
XX Sequence 1464 BP; 343 A; 405 C; 409 G; 307 T; 0 other;
XX
Query Match 16.8%; Score 324; DB 21; Length 1464;
Best Local Similarity 99.7%; Pred. No. 1.8e-158;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1555 CAATGGTCCATTACCTGTTTCATGTCGAGACCCGCGGAGCGAAGTGGTCCCAACAGTCC 1614
Db 1090 CAATGGTCCATTACCTGTTTCATGTCGAGACCCGCGGAGCGAAGTGGTCCCAACAGTCC 1149
QY 1615 AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
Db 1150 AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1209
QY 1675 GCCAAGTCCAGAGCGCGGCGAAGTGTCTGAAATCGAGTGTCTGAAAGCAGCAGTATTTTC 1734
Db 1210 GCCAAGTCCAGAGCGCGGCGAAGTGTCTGAAATCGAGTGTCTGAAAGCAGCAGTATTTTC 1269
QY 1735 CAAGGAGTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1794
Db 1270 CAAGGAGTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1329
QY 1795 AGAACGCCGTTCAAGTGTGTCTATTCTTCTGGTGGAGCAGCAGTCTTTAGTTTGGAAAGG 1854
Db 1330 AGAACGCCGTTCAAGTGTGTCTATTCTTCTGGTGGAGCAGCAGTCTTTAGTTTGGAAAGG 1389
QY 1855 TATATGGAAGGGCCATACATCGGTCAACGAGGTGCTGCAGAACTTGTGGCTAGCCCTG 1914
Db 1390 TATATGGAAGGGCCATACATCGGTCAACGAGGTGCTGCAGAACTTGTGGCTAGCCCTG 1449
QY 1915 GTGCCAGCAGCATAG 1929
Db 1450 GTGCCAGCAGCATAG 1464

RESULT 11
AAZ58395
ID AAZ58395 standard; cDNA; 1673 BP.
XX
XX AAZ58395;
XX
XX 23-MAY-2000 (first entry)
XX
XX Amino polylol amine oxidase (alpha mating factor signal peptide) DNA.
XX
XX Amino polylol amine oxidase; APAO; fumonisin; mycotoxin;
KW transgenic plant; detoxification; animal feed; silage;
KW selectable marker; alpha mating factor; signal peptide; ss.
XX
XX Chimeric - Saccharomyces cerevisiae.
OS Chimeric - Exophiala spinifera.
XX
```



CC that produce mycotoxins and/or to degrade such mycotoxins (e.g. during  
 CC ensiling); for recombinant production of APAO polypeptides; as  
 CC selection markers for plant transformation; and to isolate related  
 CC sequences from other organisms. The APAO polypeptides are used to  
 CC degrade mycotoxins in plant materials, including expression in  
 CC engineered bacteria and fungi, e.g. rumen microflora.

XX Sequence 1673 BP; 414 A; 430 C; 456 G; 373 T; 0 other;

Query Match 16.8%; Score 324; DB 21; Length 1673;  
 Best Local Similarity 99.7%; Pred. No. 1.8e-158;  
 Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCAACAGTCC 1614  
 DB 1291 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCAACAGTCC 1350  
 QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674  
 DB 1351 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1410  
 QY 1675 GCCCAAGTCCAGAGCGGCAACGTCGCTCGAAATCGAGTGTGGAAGCAGCAGTATTTC 1734  
 DB 1411 GCCCAAGTCCAGAGCGGCAACGTCGCTCGAAATCGAGTGTGGAAGCAGCAGTATTTC 1470  
 QY 1735 CAAGGAGTCCGAGCGCGCTATATGGCTGAACGATCTCATCACACTGGTTCGCGCTC 1794  
 DB 1471 CAAGGAGTCCGAGCGCGCTATATGGCTGAACGATCTCATCACACTGGTTCGCGCTC 1530  
 QY 1795 AGAAGCGCGTTCAAGTGTGTTCATTTCGTTGGAACGAGACGCTCTTATGTTGGAAGGG 1854  
 DB 1531 AGAAGCGCGTTCAAGTGTGTTCATTTCGTTGGAACGAGACGCTCTTATGTTGGAAGGG 1590  
 QY 1855 TATATGGAAGGGCCATACGATCGGCTCAACGAGTGTCTGAGAGTGTCTGGCTAGCCCTG 1914  
 DB 1591 TATATGGAAGGGCCATACGATCGGCTCAACGAGTGTCTGAGAGTGTCTGGCTAGCCCTG 1650  
 QY 1915 GTGCCAGCAGCATAG 1929  
 DB 1651 GTGCCAGCAGCATAG 1665

## RESULT 13

AAZ58402  
 ID AAZ58402 standard; cDNA; 1803 BP.

XX AAZ58402;

XX 23-MAY-2000 (first entry)

XX Exophiala spinifera amino polyol amine oxidase cDNA.

XX Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;  
 KW detoxification; animal feed; silage; selectable marker; ds.

XX Exophiala spinifera.

XX WO200004159-A1.

XX 27-JAN-2000.

XX 08-JUL-1999; 99WO-US15454.

XX 15-JUL-1998; 98US-0092936.

XX 21-MAY-1999; 99US-0135391.

XX (PION-) PIONEER HI-BRED INT INC.

XX (CURA-) CURAGEN CORP.

XX Duvick JP, Gilliam JT, Maddox JR;

XX WPI; 2000-182425/16.

XX P-PSDB; AAY58913.

XX New isolated polynucleotides, polypeptides useful for detecting and  
 PT degrading fumonisin or structurally related mycotoxin in processed  
 PT grain or in silage -  
 XX Example 10; Page 97-100; 154pp; English.

XX The present sequence is that of the coding region of full-length  
 CC amino polyol amine oxidase (APAO) cDNA of *Exophiala spinifera*  
 CC 2141.10. APAO is capable of degrading fumonisin, its hydrolysis  
 CC product API, and related mycotoxins. The invention provides APAO  
 CC polynucleotides (see AAY58383-87) and polypeptides (see AAY58900-05) of  
 CC *E. spinifera* and rhinocycliella atrovirens. The polynucleotides are  
 CC used to transform plant cells normally susceptible to Fusarium or  
 CC other toxin-producing fungus infection. Transgenic plants can be  
 CC regenerated from the transformed plant cells. Also provided are  
 CC methods for expressing both APAO and a fumonisin-esterase in a  
 CC transgenic plant, and for producing APAO enzyme in prokaryotic and  
 CC non-plant eukaryotic systems. Transgenic plants capable of degrading  
 CC fumonisin or of producing the degrading enzymes are provided.  
 CC Methods for detoxification of grain, grain processing, silage, food  
 CC crops and in animal feed and rumen microorganisms are also disclosed.  
 CC APAO polynucleotide is also useful as a selectable marker.

XX Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;

Query Match 16.8%; Score 324; DB 21; Length 1803;  
 Best Local Similarity 99.7%; Pred. No. 1.8e-158;  
 Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCAACAGTCC 1614  
 DB 1429 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCAACAGTCC 1488  
 QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674  
 DB 1489 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1548  
 QY 1675 GCCCAAGTCCAGAGCGGCAACGTCGCTCGAAATCGAGTGTGGAAGCAGCAGTATTTC 1734  
 DB 1549 GCCCAAGTCCAGAGCGGCAACGTCGCTCGAAATCGAGTGTGGAAGCAGCAGTATTTC 1608  
 QY 1735 CAAGGAGTCCGAGCGCGCTATATGGCTGAACGATCTCATCACACTGGTTCGCGCTC 1794  
 DB 1609 CAAGGAGTCCGAGCGCGCTATATGGCTGAACGATCTCATCACACTGGTTCGCGCTC 1668  
 QY 1795 AGAAGCGCGTTCAAGTGTGTTCATTTCGTTGGAACGAGACGCTCTTATGTTGGAAGGG 1854  
 DB 1669 AGAAGCGCGTTCAAGTGTGTTCATTTCGTTGGAACGAGACGCTCTTATGTTGGAAGGG 1728  
 QY 1855 TATATGGAAGGGCCATACGATCGGCTCAACGAGTGTCTGAGAGTGTCTGGCTAGCCCTG 1914  
 DB 1729 TATATGGAAGGGCCATACGATCGGCTCAACGAGTGTCTGAGAGTGTCTGGCTAGCCCTG 1788  
 QY 1915 GTGCCAGCAGCATAG 1929  
 DB 1789 GTGCCAGCAGCATAG 1803

## RESULT 14

AAZ60641  
 ID AAZ60641 standard; DNA; 1803 BP.

XX AAZ60641;

XX 16-MAY-2000 (first entry)

XX DNA encoding a full length aminopolyol amine oxidase APAO.

XX Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;  
 KW plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.

XX Exophiala spinifera.

```
XX Key Location/Qualifiers
FH 1..1803
FT /*tag= a
FT /product= "aminopolylol amine oxidase"
XX
PN WO200004160-A1.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15455.
XX
XX 15-JUL-1998; 98US-0092936.
XX
XX (PTON-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182426/16.
XX P-PSDB; AAY68849.
XX
XX New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to
XX generate plants resistant to Fusarium -
XX
XX Example 10; Page 99-101; 145pp; English.
XX
XX The present sequence encodes a full length Exophiala spinifera
XX aminopolylol amine oxidase (APAO). The enzyme has homology to the
XX flavin containing amine oxidase family, that oxidise primary amine
XX to an aldehyde or ketone, releasing ammonia and hydrogen peroxide.
XX The APAO enzyme degrades mycotoxins that promote fungal invasion of
XX plants. Destruction of mycotoxins by APAO generates, as a by-product,
XX hydrogen peroxide which is itself an antimicrobial and stimulates the
XX plants own defensive systems. The APAO polynucleotides are used to
XX generate plants (particularly maize) that are resistant to Fusarium or
XX other fungi that produce mycotoxins and/or to degrade such mycotoxins
XX (e.g. during ensilaging); for recombinant production of APAO
XX polypeptides; as selection markers for plant transformation; and to
XX isolate related sequences from other organisms. The APAO polypeptides
XX are used to degrade mycotoxins in plant materials, including expression
XX in engineered bacteria and fungi, e.g. rumen microflora.
XX
XX Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;
XX
XX Query Match 16.8%; Score 324; DB 21; Length 1803;
XX Best Local Similarity 99.7%; Pred. No. 1.8e-158;
XX Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1555 CAATGGTCCATTACCTGTTTCATGGTGGGAGACCGCGGACGAGTGGTCCCAACAGTCC 1614
XX
XX 1429 CAATGGTCCATTACCTGTTTCATGGTGGGAGACCGCGGACGAGTGGTCCCAACAGTCC 1488
XX
XX 1615 AGCAGGTACCAAAAGTGTCTGGGACCACTCCGGGAGCTACGAGAACGCCGGG 1674
XX
XX 1489 AGCAGGTACCAAAAGTGTCTGGGACCACTCCGGGAGCTACGAGAACGCCGGG 1548
XX
XX 1675 GCCCAAGTCCAGAGCCGCGCAACGTCGTAATCGAGTGGTGGAGCAGCAGTATTC 1734
XX
XX 1549 GCCCAAGTCCAGAGCCGCGCAACGTCGTAATCGAGTGGTGGAGCAGCAGTATTC 1608
XX
XX 1735 CAAGGAGTCCAGAGCGGCGTCTATGGGCTGAACGATCTCATCACTGGTTCGGCGCTC 1794
XX
XX 1609 CAAGGAGTCCAGAGCGGCGTCTATGGGCTGAACGATCTCATCACTGGTTCGGCGCTC 1668
XX
XX 1795 AGAAGCCGTTCAAGTGTGTTCATCTTCGTTGGAGGAGACGCTTTAGTTGGAAAGGG 1854
XX
XX 1669 AGAAGCCGTTCAAGAGTGTTCATCTTCGTTGGAGGAGACGCTTTAGTTGGAAAGGG 1728
XX
XX 1855 TATATGAAGGGGCGCATACGATCGGCTCAACGAGTGTCTGCAAGAGTGTGGCTAGCGCTG 1914
XX
XX 1729 TATATGAAGGGGCGCATACGATCGGCTCAACGAGTGTCTGCAAGAGTGTGGCTAGCGCTG 1788
XX
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Qy 1915 GTCCAGCAGCATAG 1929
Dy 1789 GTCCAGCAGCATAG 1803
AAZ58384
ID AAZ58384 standard; DNA; 1930 BP.
AC AAZ58384;
XX
XX 23-MAY-2000 (first entry)
XX
XX Exophiala spinifera amino polyol amine oxidase ESP003_C12 DNA.
XX
XX Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;
XX detoxification; animal feed; silage; selectable marker; ds.
XX
XX Exophiala spinifera.
XX
XX Key Location/Qualifiers
FH 1..1930
FT CDS
FT /*tag= a
FT /note= "contains introns"
FT intron 739..811
FT /*tag= b
FT intron 1134..1187
FT /*tag= c
XX
XX WO200004159-A1.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15454.
XX
XX 15-JUL-1998; 98US-0092936.
XX 21-MAY-1999; 99US-0135391.
XX
XX (PTON-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Duvick JP, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182425/16.
XX P-PSDB; AAY58902.
XX
XX New isolated polynucleotides, polypeptides useful for detecting and
XX degrading fumonisins or structurally related mycotoxins in processed
XX grain or in silage ;
XX
XX Claim 1; Page 141-142; 154pp; English.
XX
XX The present sequence is that of an isolated nucleic acid,
XX designated ESP003_C12, of Exophiala spinifera isolate ESP002,
XX which encodes an amino polyol amine oxidase (APAO, see AAY58902)
XX capable of degrading fumonisins, its hydrolysis product APL, and
XX related mycotoxins. The DNA was obtained by PCR amplification of
XX ESP003 mycelial DNA using primers based on APAO of E. spinifera
XX ATCC 74269. The invention provides APAO polynucleotides (see
XX AAY58383-87) and polypeptides (see AAY58900-05) of E. spinifera and
XX Rhinocladia atrovirens. The polynucleotides are used to transform
XX plant cells normally susceptible to Fusarium or other toxin-producing
XX fungus infection. Transgenic plants can be regenerated from the
XX transformed plant cells. Also provided are methods for expressing
XX both APAO and a fumonisin-esterase in a transgenic plant, and for
XX producing APAO enzyme in prokaryotic and non-plant eukaryotic
XX systems. Transgenic plants capable of degrading fumonisins or of
XX producing the degrading enzymes are provided. Methods for
XX detoxification of grain, grain processing, silage, food crops and
XX in animal feed and rumen microorganisms are also disclosed. APAO
XX polynucleotide is also useful as a selectable marker.
XX
XX Sequence 1930 BP; 449 A; 531 C; 537 G; 412 T; 1 other;
```

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Best Local Similarity		99.7%;	Pred No. 1.8e-158;		
Matches 374;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
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Db	1556	CAATGGTCCATTACCTGTTTCATGTCGGAGACCGCGGACCGAAGTGGTCCCAACAGTCC	1615		
QY	1615	AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCCGCAGCCTACGAGAACGCCGGG	1674		
Db	1616	AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCCGCAGCCTACGAGAACGCCGGG	1675		
QY	1675	GCCCAAGTCCAGAGCGCGCCACGCTCGAAATCGAGTGGTCGAGCAGCAGTATTTC	1734		
Db	1676	GCCCAAGTCCAGAGCGCGCCACGCTCGAAATCGAGTGGTCGAGCAGCAGTATTTC	1735		
QY	1735	CAAGGAGCTCCGAGCGCCGCTATGGGCTGAACGATCTCATCACACTGGGTTGCGCGCTC	1794		
Db	1736	CAAGGAGCTCCGAGCGCCGCTATGGGCTGAACGATCTCATCACACTGGGTTGCGCGCTC	1795		
QY	1795	AGAACGCCGTTCAAGTGTGTTTCATTTCGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGGG	1854		
Db	1796	AGAACGCCGTTCAAGTGTGTTTCATTTCGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGGG	1855		
QY	1855	TATATGGAAGGGGCCATACGATCGGTCACGAGGTGCTGCAGAGTGTGGCTAGCCTG	1914		
Db	1856	TATATGGAAGGGGCCATACGATCGGTCACGAGGTGCTGCAGAGTGTGGCTAGCCTG	1915		
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Db	1916	GTGCCAGCAGCATAG	1930		

Search completed: November 12, 2002, 05:41:50  
Job time : 425 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2002, 04:43:45 ; Search time 2811 Seconds  
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Title: US-09-771-045A-35

Perfect score: 1929

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Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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EST.\*

1: em\_estba.\*  
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8: em\_hic.\*  
9: gb\_est1.\*  
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26: em\_gss\_pro.\*  
27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	1.2	623	17 AQ280543	AQ280543 CITBI-E1-
C 2	21	1.1	1284	14 BM803905	BM803905 AGENCOURT
C 3	20	1.0	285	13 BI050480	BI050480 CM3-GN031
C 4	20	1.0	434	17 AQ046343	AQ046343 RPC111-34
C 5	20	1.0	526	17 AQ697937	AQ697937 HS.5536_B
C 6	20	1.0	716	9 AU133639	AU133639 AU133639

7	20	1.0	807	12 BG522272	BG522272
C 8	20	1.0	922	17 AG059979	AG059979 Pan trogl
9	19	1.0	80	17 BH811443	BH811443 SALK_0586
10	19	1.0	119	10 AW783945	AW783945 P2T1L6 PL
C 11	19	1.0	181	9 AL710341	AL710341 DKFZp866H
C 12	19	1.0	182	10 BE560457	BE560457 601346723
C 13	19	1.0	184	14 BQ805991	BQ805991 WHE3573_E
C 14	19	1.0	185	10 BE264866	BE264866 601194354
C 15	19	1.0	201	12 BE796178	BE796178 601591321
C 16	19	1.0	212	12 BE714854	BE714854 IL5-HT073
C 17	19	1.0	213	12 BE903091	BE903091 601677147
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C 19	19	1.0	223	12 BE714855	BE714855 IL5-HT073
C 20	19	1.0	225	12 BG386968	BG386968 602455159
C 21	19	1.0	226	12 BG481342	BG481342 602528687
C 22	19	1.0	227	12 BG386339	BG386339 602455540
C 23	19	1.0	227	13 BI200064	BI200064 602760735
C 24	19	1.0	233	10 BE249908	BE249908 600942953
C 25	19	1.0	234	10 BE267669	BE267669 601124928
C 26	19	1.0	236	10 BE267625	BE267625 601124848
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C 28	19	1.0	241	12 BF306512	BF306512 601888920
C 29	19	1.0	242	12 BE899487	BE899487 601682278
C 30	19	1.0	257	10 AW672654	AW672654 ba49a02.Y
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C 33	19	1.0	297	9 AA353525	AA353525 EST62020
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38	19	1.0	355	9 AA013604	AA013604 mh25g09.r
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C 44	19	1.0	392	9 AI450161	AI450161 mt86d08.x
C 45	19	1.0	406	10 AW504032	AW504032 UI-HF-BNO

#### ALIGNMENTS

RESULT 1  
AQ280543  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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CITBI-E1-251406.TF CITBI-E1 Homo sapiens genomic clone 251406, DNA  
sequence.  
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AQ280543.1 GI:3906362  
GSS.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 623)  
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,J.C., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and  
Venner,J.C.  
Use of a random human BAC End Sequence Database for Sequence-Ready  
Map Building  
Unpublished (1998)  
Other GSSs: CITBI-E1-251406.TF  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:

http://www.tigr.org/tdb/hungen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13-21  
Class: BAC ends.

## FEATURES

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Caltech Human BAC Library D"

BASE COUNT 136 a 192 c 94 g 200 t 1 others

## ORIGIN

Query Match 1.2%; Score 23; DB 17; Length 623;  
Best Local Similarity 100.0%; Pred. No. 0.81; Mismatches 0; Indels 0; Gaps 0;  
Matches 23; Conservative 0;

Qy 783 AATACAGTCACTGACTCCACTTC 805  
|||||  
Db 139 AATACAGTCACTGACTCCACTTC 161

## RESULT-2

## BM803905/c

## LOCUS

DEFINITION BM803905 1284 bp mRNA linear EST 05-MAR-2002  
5', mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 1284)  
NIH-MGC http://mgc.nci.nih.gov/.

## AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

## JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs@email.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing By: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: Agencourt Bioscience Corporation

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12184 row: o column: 06

High quality sequence stop: 453.

## FEATURES

## source

Location/Qualifiers  
1..1284  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5520605"  
/clone\_lib="NIH-MGC-71"  
/tissue\_type="leiomyosarcoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="organ: uterus; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.1 kb.

BASE COUNT 260 a 382 g 362 g 276 t 4 others

## ORIGIN

Query Match 1.1%; Score 21; DB 14; Length 1284;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 CGTGGTAGTGGCGCTGG 449

Db 1196 CGTGGTAGTGGCGCTGG 1176

## RESULT 3

## BI050480/c

## LOCUS

DEFINITION CM3-GN0313-050101-593-e06 GN0313 Homo sapiens cDNA, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

1 (bases 1 to 285)  
Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

## sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## JOURNAL

## MEDLINE

## COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

{http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0313-

050101-593-e06&t3=2001-01-05&t4=1}

Seq primer: puc 18 forward

High quality sequence start: 8

High quality sequence stop: 285.

## FEATURES

## source

Location/Qualifiers  
1..285  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="GN0313"  
/dev\_stage="Adult"  
/note="organ: placenta\_normal; Vector: puc18; Site\_1: SmaI  
; Site\_2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the puc 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."

BASE COUNT 73 a 70 c 53 g 89 t

## ORIGIN

Query Match 1.0%; Score 20; DB 13; Length 285;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1625 GACAAAGTCTGTCTGGGAC 1644

Db 173 GACAAAGTCTGTCTGGGAC 154

## RESULT 4

## AQ046343/c

## LOCUS

DEFINITION AQ046343 434 bp DNA linear GSS 14-APR-1999  
RPC111-34118.TK RPCI-11 Homo sapiens genomic clone RPCI-11-34118,

## DNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

human.



```

ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               1 (bases 1 to 434)
ADAMS,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
TITLE          Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL        Unpublished (1998)
COMMENT        Contact: Mark Adams
               Department of Eukaryotic Genomics
               The Institute for Genomic Research
               9712 Medical Center Dr., Rockville, MD 20850, USA
               Tel: 301 838 0200
               Fax: 301 838 0208
               Email: mdadams@tigr.org
               Clones are derived from the human BAC library RPCI-11. For BAC
               library availability, please contact Pieter de Jong
               (pieter@dejong.med.buffalo.edu). Clones may be purchased from
               BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
               Research Genetics (info@resgen.com). BAC end search page:
               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
               Class: BAC ends.
               Location/Qualifiers
                 1..434
                 /organism="Homo sapiens"
                 /db_xref="GDB:7512881"
                 /db_xref="taxon:9606"
                 /clone="RPCI-11-34118"
                 /clone_lib="RPCI-11"
                 /sex="Male"
                 /cell_type="Lymphocytes"
                 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
                 RPC11 Human Male BAC Library"
BASE COUNT    119 a 90 c 80 g 145 t
ORIGIN
Query Match      1.0%; Score 20; DB 17; Length 434;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1176 GGTCAATCCAGTATGCAGT 1195
      |||||
Db 190 GGTCAATCCAGTATGCAGT 171

RESULT 5
LOCUS      AQ697937      526 bp      DNA      linear      GSS      06-JUL-1999
DEFINITION      HS_5536_B1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens
                genomic clone Plate=1112 Col=17 Row=N, DNA sequence.
ACCESSION      AQ697937
VERSION        AQ697937.1 GI:5388185
KEYWORDS       GSS.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               1 (bases 1 to 526)
               Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
               Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
               Hood,L.
TITLE          Sequence-tagged connectors: A sequence approach to mapping and
               scanning the human genome
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE        99380589
COMMENT        Contact: Mahairas GG, Wallace JC, Hood L
               High Throughput Sequencing Center
               University of Washington
               401 Queen Anne Avenue North, Seattle, WA 98109, USA
               Tel: (206) 616-3618
               Fax: (206) 616-3887
               Email: jwallace@u.washington.edu

```

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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1112 row: N column: 17
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 526.
Location/Qualifiers
  1..526
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="Plate=1112 Col=17 Row=N"
  /clone_lib="RPCI-11 Human Male BAC Library"
  /sex="male"
  /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"
BASE COUNT    159 a 104 c 76 g 185 t
ORIGIN
Query Match      1.0%; Score 20; DB 17; Length 526;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1358 ATCCACCTTGACATTTC 1377
      |||||
Db 403 ATCCACCTTGACATTTC 422

RESULT 6
LOCUS      AU133639/c      716 bp      mRNA      linear      EST 01-AUG-2002
DEFINITION      AU133639 OVARC1 Homo sapiens cDNA clone OVARC1000332 5', mRNA
                sequence.
ACCESSION      AU133639
VERSION        AU133639.1 GI:10994178
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               1 (bases 1 to 716)
               Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
               Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
               Isogai,T.
TITLE          HRI human cDNA project
JOURNAL        Unpublished (2000)
COMMENT        Contact: Takao Isogai
               Genomics Laboratory
               Helix Research Institute
               1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
               Tel: 81-438-52-3975
               Fax: 81-438-52-3986
               Email: genomics@hri.co.jp
               HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
               Research Institute; cDNA library construction: Department of
               Virology, Institute of Medical Science, University of Tokyo, and
               Helix Research Institute.
Location/Qualifiers
  1..716
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="OVARC1000332"
  /clone_lib="OVARC1"
  /tissue.type="ovary, tumor tissue"
  /note="Vector: pME18SFL3"
BASE COUNT    168 a 197 c 193 g 155 t
ORIGIN

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```

Query Match      1.0%; Score 20; DB 9; Length 716;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACGCCGGGGCCCAAGTCCCA 1686
DB 79 ACGCCGGGGCCCAAGTCCCA 60

RESULT 7
LOCUS      BG522272
DEFINITION 2-42 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
ACCESSION  BG522272
VERSION     BG522272.1 GI:18465336
KEYWORDS   EST.
SOURCE     Stevia rebaudiana.
ORGANISM   Stevia rebaudiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
Heliantheae; Stevia.
1 (bases 1 to 807)
REFERENCE  Brandle, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.
AUTHORS   Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in
TITLE     diterpene synthesis
JOURNAL   Unpublished (2001)
COMMENT   Contact: Jim Brandle
           Genomics and Biotechnology
           Agriculture and Agri-Food Canada - SCPPRC
           1391 Sandford St., London, Ontario, CANADA, N5V 4T3
           Tel: 519 457 1470
           Fax: 519 457 3997
           Email: brandleje@em.agr.ca
           Seq primer: T3 promoter primer.
           Location/Qualifiers
             1..807
               /organism="Stevia rebaudiana"
               /strain="751/1501"
               /cultivar="Landrace"
               /db_xref="taxon:55670"
               /clone_lib="Stevia field grown leaf cDNA"
               /dev_stage="field grown, mid-size"
               /tissue_type="leaf"
               /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from field grown leaves. Mid-size actively growing leaves
were collected and pooled from several plants and frozen
immediately after harvesting in liquid nitrogen. The cDNA
was prepared using an XhoI-poly(dT) linker-primer. An
EcoRI adapter was ligated to the blunt end cDNA and the
products were digested with EcoRI and XhoI enabling
directional cloning into the lambda ZAP Express vector.
The library was amplified using the host strain XL1-Blue
MRF'. Mass excision of the library was performed to
obtain pBK-CMV phagemid clones in the host strain XL0LR.
Single pass DNA sequencing was performed using the T3
promoter primer: 5' ATTACCCCTCAAGGGA 3'. This library
was constructed by Alex Richman."
BASE COUNT      245 a 144 c 179 g 232 t 7 others
ORIGIN

Query Match      1.0%; Score 20; DB 12; Length 807;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 GAGTTGCAAGTCGACTTGC 840
DB 355 GAGTTGCAAGTCGACTTGC 374

RESULT 8
LOCUS      AG059979/c
DEFINITION Pan troglodytes DNA, clone: PTB-047F09.R, genomic survey sequence.
ACCESSION  AG059979
VERSION     AG059979.1 GI:16611209
KEYWORDS   GSS.
SOURCE     Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
ORGANISM   Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 922)
REFERENCE  Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
AUTHORS   Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE     Direct Submission
JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
[E-mail:chmpes@gs.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170]
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector      : pKS145
R.Site 1    : SacI
R.Site 2    : SacI.
Location/Qualifiers
  1..922
    /organism="Pan troglodytes"
    /db_xref="taxon:9598"
    /clone="PTB-047F09.R"
    /sex="male"
    /cell_type="lymphoblast"
    /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT    51 a 271 c 355 g 243 t 2 others
ORIGIN

Query Match      1.0%; Score 20; DB 17; Length 922;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 CCACATCGCGGTAGGCCCA 78
DB 740 CCACATCGCGGTAGGCCCA 721

RESULT 9
LOCUS      BH811443
DEFINITION SALK_058617 Arabidopsis thaliana T-DNA insertion lines Arabidopsis
thaliana genomic clone SALK_058617, DNA sequence.
ACCESSION  BH811443
VERSION     BH811443.1 GI:20389898
KEYWORDS   GSS.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; euroids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 80)
REFERENCE  Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab
AUTHORS   , C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
           Zimmerman, J. and Ecker, J.R.

```

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g47210 and an annotated exon of At1g47210.  
Class: TDNA tagged.

FEATURES Location/Qualifiers

1..80

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_058617"

/note="PCR was performed on Arabidopsis thaliana lines"

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

14 a 22 c 15 g 29 t

BASE COUNT

ORIGIN

Query Match 1.0%; Score 19; DB 17; Length 80;

Best Local Similarity 100.0%; Pred. NO. 82;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 GCCTTGGCTTACCTGAAT 364

|||||

Db 61 GCCTTGGCTTACCTGAAT 79

RESULT 10

AW783945

LOCUS

DEFINITION P21116 Plasmodium yoelii infected liver tissues EST 22-NOV-2000

Similar to liver and blood stage P. yoelii antigen, mRNA sequence.

AW783945 119 bp mRNA linear EST 22-NOV-2000

AW783945.1 GI:7838321

ACCESSION

VERSION

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 119)

Authors Lau, A.O.T., Sacchi, J.B. Jr and Azad, A.F.

Title Retrieving parasite specific liver stage gene products in

Plasmodium yoelii infected livers using differential display

Mol. Biochem. Parasitol. 111, 143-151 (2000)

JOURNAL 20542037

MEDLINE

COMMENT

Contact: Lau, AOT

Dept. of Microbiology and Immunology

University of Maryland, Baltimore

655 W. Baltimore Street, BRB 3-034, Baltimore, MD 21201, USA

Tel: 410-706-7066

Fax: 410-706-0282

Email: [alau@umaryland.edu](mailto:alau@umaryland.edu)

PCR Primers

FORWARD: TGTTATACTGTTTAC

BACKWARD: CTACAGTGGCTTAATAC

Insert Length: 119 Std Error: 0.00.

Location/Qualifiers

1..119

/organism="Mus musculus"

/strain="BALB/c"

/db\_xref="taxon:10090"

FEATURES

Source

/clone\_lib="Plasmodium yoelii infected liver tissues"  
/tissue\_type="liver"  
/note="Organ: liver; P. yoelii sporozoites were IV  
injected into BALB/c mice and livers were harvested 24  
hours post injection. Total RNA was processed and  
differential display was performed on the infected liver  
samples along with uninfected BALB/c liver control."  
BASE COUNT 31 a 16 c 19 g 53 t  
ORIGIN

Query Match 1.0%; Score 19; DB 10; Length 119;

Best Local Similarity 100.0%; Pred. NO. 89;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1803 GTTCAAGTGCTTCATTC 1821

|||||

Db 43 GTTCAAGTGCTTCATTC 61

RESULT 11

AL710341/c

LOCUS

DEFINITION DKFZp686h1969\_r1 686 (synonym: hlcc3) Homo sapiens CDNA clone

DKFZp686h1969\_5', mRNA sequence.

AL710341 181 bp mRNA linear EST 22-MAR-2002

ACCESSION

VERSION

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 181)

Authors Ansong, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.

Title EST (Ansong, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)

JOURNAL Unpublished (1999)

COMMENT Contact: Ansong W

MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: [s.wiemann@dkfz-heidelberg.de](mailto:s.wiemann@dkfz-heidelberg.de);

sequenced by EMBL (European Molecular Biology Laboratories,

Heidelberg/Germany) within the CDNA sequencing consortium of the

German Genome Project.

No si sequence available.

This clone (DKFZp686h1969) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: [clone@rzpd.de](mailto:clone@rzpd.de).

FEATURES

Source

1..181

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="DKFZp686h1969"

/clone\_lib="686 (synonym: hlcc3)"

/tissue\_type="human skeletal muscle"

/dev\_host="adult"

/lab\_host="DH10B"

/note="vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiIb;

CDNA-collection"

BASE COUNT 26 a 57 c 64 g 31 t 3 others

ORIGIN

Query Match 1.0%; Score 19; DB 9; Length 181;

Best Local Similarity 100.0%; Pred. NO. 98;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGCCCAAGTCCCA 1686

|||||

Db 66 CGCCGGGCCCAAGTCCCA 48

RESULT 12

BE560457/c

LOCUS BE560457 182 bp mRNA linear EST 15-AUG-2000  
 DEFINITION 601346723f1 NIH\_MGC\_8 Homo sapiens cDNA clone IMAGE:3687725 5',  
 mRNA sequence.  
 ACCESSION BE560457  
 VERSION BE560457.1 GI:9804177  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 182)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb@mail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: MGC Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: LICM379 row: m column: 06  
 High quality sequence start: 3  
 High quality sequence stop: 182.  
 Location/Qualifiers  
 1..182  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3687725"  
 /clone\_lib="NIH\_MGC\_8"  
 /tissue\_type="Burkitt lymphoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: lymph; Vector: pOR7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dr priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 BASE COUNT 26 a 65 c 60 g 31 t  
 ORIGIN  
 Query Match 1.0%; Score 19; DB 10; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1668 CGCCGGGCCCAAGTCCCA 1686  
 |||||  
 Db 34 CGCCGGGCCCAAGTCCCA 16  
 RESULT 13  
 BQ805991 184 bp mRNA linear EST 31-JUL-2002  
 LOCUS WHE35733\_E02\_J03S2 wheat developing grains cDNA library Triticum  
 DEFINITION aestivum cDNA clone WHE35733\_E02\_J03, mRNA sequence.  
 ACCESSION BQ805991  
 VERSION BQ805991.1 GI:22030200  
 KEYWORDS EST.  
 SOURCE bread wheat.  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae  
 ; Triticeae; Triticum.  
 1 (bases 1 to 184)  
 Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin  
 K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J.,  
 Wilson, C. and Woo, J.  
 The structure and function of the expressed portion of the wheat  
 genomes - Developing grains cDNA library  
 Unpublished (2002)

COMMENT Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105595773  
 Fax: 5105595818  
 Email: oanderson@pw.usda.gov  
 Sequences have been trimmed to remove vector sequence and low  
 quality sequence with phred score less than 20  
 Seq primer: SK primer.  
 FEATURES  
 1..184  
 Location/Qualifiers  
 source  
 /organism="Triticum aestivum"  
 /cultivar="Butte 86"  
 /db\_xref="taxon:4565"  
 /clone="WHE35733\_E02\_J03"  
 /clone\_lib="Wheat developing grains cDNA library"  
 /tissue\_type="whole grains"  
 /dev\_stage="3-44 days post anthesis seed"  
 /lab\_host="E. coli SOLR"  
 /note="Vector: Lambda ZAP II, excised phagemid; Site\_1:  
 EcoRI; Plants were grown under six following different  
 environmental regimes in greenhouse. Environment 1)  
 240C/170C day/night, well-watered, with post-anthesis  
 fertilizer, Environment 2) 240C/170C day/night,  
 well-watered, without post-anthesis fertilizer,  
 Environment 3) 370C/170C day/night, well-watered, with  
 post-anthesis fertilizer, Environment 4) 370C/170C  
 day/night, well-watered, without post-anthesis fertilizer,  
 Environment 5) 370C/170C day/night plus drought, with  
 post-anthesis fertilizer, Environment 6) 370C/170C  
 day/night plus drought, without post-anthesis fertilizer,  
 developing wheat grains from the following were excised  
 and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,  
 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment  
 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44  
 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28,  
 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24,  
 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16,  
 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16,  
 20, 24, 28, 30 DPA and total RNA was prepared by S.  
 Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA  
 library was made using poly (A) RNA, and the cDNA clones  
 were in vivo excised to give pBluescript SK(-) phagemids  
 in the TJ Close lab (Chin, Close, Fenton) at the  
 University of California, Riverside. Plasmid DNA  
 preparations and DNA sequencing were performed in the OD  
 Anderson lab (others)."  
 BASE COUNT 32 a 47 c 49 g 56 t  
 ORIGIN  
 Query Match 1.0%; Score 19; DB 14; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 187 GCTTGCCTTCTGCAGTTG 205  
 |||||  
 Db 108 GCTTGCCTTCTGCAGTTG 126  
 RESULT 14  
 BE264866/c 185 bp mRNA linear EST 13-JUL-2000  
 LOCUS 601194354f1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:3538309 5',  
 mRNA sequence.  
 DEFINITION BE264866  
 ACCESSION BE264866  
 VERSION BE264866.1 GI:9138427  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 185)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Plate: LLCM223 row: k column: 14  
 High quality sequence start: 4  
 High quality sequence stop: 185.

FEATURES  
 source  
 1..185  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3538309"  
 /clone\_lib="NIH\_MGC\_7"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 26 a 64 c 61 g 34 t  
 ORIGIN

Query Match 1.0%; Score 19; DB 10; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1686  
 |||||  
 Db 37 CGCCGGGGCCCAAGTCCCA 19

RESULT 15  
 BE796178/c  
 LOCUS BE796178 201 bp mRNA linear EST 20-SEP-2000  
 DEFINITION 601591321F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:3945316 5',  
 mRNA sequence.  
 BE796178  
 VERSION BE796178.1 GI:10217376  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 201)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: LLCM803 row: j column: 05  
 High quality sequence stop: 201.

FEATURES  
 source  
 1..201  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3945316"  
 /clone\_lib="NIH\_MGC\_7"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 27 a 72 c 66 g 36 t  
 ORIGIN

Query Match 1.0%; Score 19; DB 12; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1686  
 |||||  
 Db 53 CGCCGGGGCCCAAGTCCCA 35

Search completed: November 12, 2002, 06:28:56  
 Job time : 2820 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: November 12, 2002, 04:43:45 ; Search time 2811 Seconds  
(without alignments)  
11113.872 Million cell updates/sec

Title: US-09-771-045A-35  
Perfect score: 1929  
Sequence: 1 atgacctgaccagagcta.....gctgtgcccagcagcatag 1929

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Databaŕe :

- EST.\*
- 1: em\_estba.\*
  - 2: em\_esthum.\*
  - 3: em\_estlin.\*
  - 4: em\_estm.\*
  - 5: em\_estov.\*
  - 6: em\_estpl.\*
  - 7: em\_estro.\*
  - 8: em\_hic.\*
  - 9: gb\_estl.\*
  - 10: gb\_est2.\*
  - 11: gb\_hic.\*
  - 12: gb\_est3.\*
  - 13: gb\_est4.\*
  - 14: gb\_est5.\*
  - 15: em\_estfun.\*
  - 16: em\_estom.\*
  - 17: gb\_gss.\*
  - 18: em\_gss\_hum.\*
  - 19: em\_gss\_inv.\*
  - 20: em\_gss\_pln.\*
  - 21: em\_gss\_vrt.\*
  - 22: em\_gss\_fun.\*
  - 23: em\_gss\_mam.\*
  - 24: em\_gss\_mus.\*
  - 25: em\_gss\_other.\*
  - 26: em\_gss\_pro.\*
  - 27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	1.2	623	17	AQ280543
2	21	1.1	1284	14	BM803905
3	20	1.0	285	13	BI050480
4	20	1.0	434	17	AQ046343
5	20	1.0	526	17	AQ697937
6	20	1.0	716	9	AU133639

7	1.0	807	12	BG522272	2-42 Stev
8	1.0	922	17	AG059979	AG059979 Pan trogl
9	1.0	80	17	BH811443	BH811443 SALK_0586
10	1.0	119	10	AW783945	AW783945 P2T1L6 PL
11	1.0	181	9	AL710341	AL710341 DKE2P686H
12	1.0	182	10	BE560457	BE560457 601346723
13	1.0	184	14	BQ805991	BQ805991 WHE3373-E
14	1.0	185	10	BE264866	BE264866 601194354
15	1.0	201	12	BE796178	BE796178 601591321
16	1.0	212	12	BE714854	BE714854 IL5-HT073
17	1.0	213	12	BE903091	BE903091 601677147
18	1.0	218	12	BE204571	BE204571 601868184
19	1.0	223	12	BE714855	BE714855 IL5-HT073
20	1.0	225	12	BG386968	BG386968 602455159
21	1.0	226	12	BG481342	BG481342 602528687
22	1.0	227	12	BG386339	BG386339 602455540
23	1.0	227	13	BI200064	BI200064 602760735
24	1.0	233	10	BE249908	BE249908 600942953
25	1.0	234	10	BE267669	BE267669 601124928
26	1.0	236	10	BE267625	BE267625 601124848
27	1.0	240	12	BF308488	BF308488 601887626
28	1.0	241	12	BF306512	BF306512 601888920
29	1.0	242	12	BE899487	BE899487 601682278
30	1.0	257	10	AW672654	AW672654 ba49a02.Y
31	1.0	268	14	BM835102	BM835102 K-EST0110
32	1.0	295	12	BG152936	BG152936 nah95b10
33	1.0	297	9	AA353525	AA353525 ES62020
34	1.0	319	9	AI414414	AI414414 mb01906.x
35	1.0	328	10	BE380159	BE380159 601186753
36	1.0	331	9	AA479264	AA479264 zv17h04.r
37	1.0	333	17	BH317104	BH317104 CH230-196
38	1.0	355	9	AA013604	AA013604 mh25q09.r
39	1.0	355	9	AI415050	AI415050 mb89b09.x
40	1.0	369	14	BM829459	BM829459 K-EST0102
41	1.0	373	9	AA542887	AA542887 ni98a02.s
42	1.0	373	13	BI005958	BI005958 CM2-RT006
43	1.0	390	14	BM755698	BM755698 K-EST0033
44	1.0	392	9	AI450161	AI450161 mt86d08.x
45	1.0	406	10	AW504032	AW504032 UI-HF-BN0

## ALIGNMENTS

RESULT 1  
AQ280543  
LOCUS  
DEFINITION  
CITBI-E1-251406.TF CITBI-E1 Homo sapiens genomic clone 251406, DNA linear GSS 22-NOV-1998  
sequence.  
ACCESSION  
AQ280543  
VERSION  
AQ280543.1  
KEYWORDS  
GSS.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 623)  
AUTHORS  
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Barry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.  
TITLE  
Use of a random human BAC End Sequence Database for Sequence-Ready Map Building  
JOURNAL  
Unpublished (1998)  
COMMENT  
Other GSSs: CITBI-E1-251406.TR  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC end search page:





http://www.tigr.org/tldb/humgen/bac\_end\_search/bac\_end\_search.html.

Seq primer: M13-21

Class: BAC ends.

## FEATURES

Source  
Location/Qualifiers  
1..623  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="251406"  
/clone\_lib="CITBI-E1"  
/sex="male"  
/cell\_type="sperm"  
/note="Vector: pBelobAC11; Site\_1: EcoRI; Site\_2: EcoRI;  
Caltech Human BAC Library D"

BASE COUNT 136 a 192 c 94 g 200 t 1 others

## ORIGIN

Query Match 1.2%; Score 23; DB 17; Length 623;  
Best Local Similarity 100.0%; Pred. No. 0.81; Mismatches 0; Indels 0; Gaps 0;  
Matches 23; Conservative 0;

QY 783 AATACAGTCACTGACTCCACTTC 805

Db 139 AATACAGTCACTGACTCCACTTC 161

## RESULT-2

BM803905/c

## LOCUS

DEFINITION BM803905 1284 bp mRNA linear EST 05-MAR-2002  
AGENCOURT.6439488 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:5520605

## ACCESSION

VERSION BM803905.1 GI:19120728

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

## REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CNA Library Preparation: Life Technologies, Inc.

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12184 row: o column: 06

High quality sequence stop: 453.

Location/Qualifiers

1..1284

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5520605"

/clone\_lib="NIH\_MGC\_71"

/tissue\_type="leiomyosarcoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 2.1 kb.

BASE COUNT 260 a 382 c 362 g 276 t 4 others

## ORIGIN

Query Match 1.1%; Score 21; DB 14; Length 1284;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

429 CCGTGTAGTGGTGGCGGTGG 449

|||||

96 CCGTGTAGTGGTGGCGGTGG 1176

## RESULT 3

BI050480/c

## LOCUS

DEFINITION CM3-GN0313-050101-593-e06 GN0313 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI050480

VERSION BI050480.1 GI:14458010

KEYWORDS EST.

SOURCE human.

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 285)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0313-

050101-593-e06&t3=2001-01-05&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 8

High quality sequence stop: 285.

Location/Qualifiers

1..285

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="GN0313"

/dev\_stage="Adult"

/note="Organ: placenta; normal; Vector: puc18; Site\_1: SmaI

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the puc 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT 73 a 70 c 53 g 89 t

## ORIGIN

Query Match 1.0%; Score 20; DB 13; Length 285;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1625 GACAAAGTCTGTCTGGGAC 1644

|||||

Db 173 GACAAAGTCTGTCTGGGAC 154

## RESULT 4

AQ046343/c

## LOCUS

DEFINITION RPC111-34118-TK RPC1-11 Homo sapiens genomic clone RPCI-11-34118,

DNA sequence.

ACCESSION AQ046343

VERSION AQ046343.1 GI:3315270

KEYWORDS GSS.

SOURCE human.





QY 241 TATACGTGCTAGTCCCGCCGAGCAAACTACCGCAATTGGAGTGGCTGAAGTCTACC 300  
Db 241 TATACGTGCTAGTCCCGCCGAGCAAACTACCGCAATTGGAGTGGCTGAAGTCTACC 300  
QY 301 TTTGGCCTTGACAGGCTCCCTCTTGGCAGCTGGTGGCAGTACCGGCCCTTGGCTTCACCT 360  
Db 301 TTTGGCCTTGACAGGCTCCCTCTTGGCAGCTGGTGGCAGTACCGGCCCTTGGCTTCACCT 360  
QY 361 GAATACCTCTTTGAGGTTGATCCACGCGCTGGTGGCAGGACACTCGACCCGACACAC 420  
Db 361 GAATACCTCTTTGAGGTTGATCCACGCGCTGGTGGCAGGACACTCGACCCGACACAC 420  
QY 421 GTTGGCAGCTGGTATGTTGGCGCTGGCTTGGAGCGGTTTGGAGACGCGACGAAAGTC 480  
Db 421 GTTGGCAGCTGGTATGTTGGCGCTGGCTTGGAGCGGTTTGGAGACGCGACGAAAGTC 480  
QY 481 CAGGCCCGCGTCTGTCTTGGCGCTGGCTTGGAGCGGTTTGGAGCGGTTTGGAGCGGTT 540  
Db 481 CAGGCCCGCGTCTGTCTTGGCGCTGGCTTGGAGCGGTTTGGAGCGGTTTGGAGCGGTT 540  
QY 541 CTGAGGTTACAACTCGGTTCCCGGAGGAGGACTATCAAGGACCTCGCGCTCGGTGGATC 600  
Db 541 CTGAGGTTACAACTCGGTTCCCGGAGGAGGACTATCAAGGACCTCGCGCTCGGTGGATC 600  
QY 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGGCGAG 660  
Db 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGGCGAG 660  
QY 661 CTCGAGGACGACCGGAAATTCATTCATCAAGCAGAGCGGTACACCACTACAGCT 720  
Db 661 CTCGAGGACGACCGGAAATTCATTCATCAAGCAGAGCGGTACACCACTACAGCT 720  
QY 721 CCTATGTTGACTCCCGGTAAAGCAATCCACATTTGTTGATGAGACCTCTGTCCAGTGT 780  
Db 721 CCTATGTTGACTCCCGGTAAAGCAATCCACATTTGTTGATGAGACCTCTGTCCAGTGT 780  
QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCATTTGC 840  
Db 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCATTTGC 840  
QY 841 GGAATCTCTCCCGTATGTTCTCAGCTGATCGAAGAGTATAGCCTTGAAGCCCCAAGGC 900  
Db 841 GGAATCTCTCCCGTATGTTCTCAGCTGATCGAAGAGTATAGCCTTGAAGCCCCAAGGC 900  
QY 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAGGAGCT 960  
Db 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAGGAGCT 960  
QY 961 AAATTTGCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGGA 1020  
Db 961 AAATTTGCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGGA 1020  
QY 1021 AGCCGAGAGATCAGGATGCTTTTCTCACCAGCTACATCAAGAGTGGCAGCGTCTCAG 1080  
Db 1021 AGCCGAGAGATCAGGATGCTTTTCTCACCAGCTACATCAAGAGTGGCAGCGTCTCAG 1080  
QY 1081 TAATATGTTCTCGGCAAGAAAGCGGCGAGTATATGCCATCAAAACAGTGGCGTG 1140  
Db 1081 TAATATGTTCTCGGCAAGAAAGCGGCGAGTATATGCCATCAAAACAGTGGCGTG 1140  
QY 1141 CGGTGCTCTCAGGTAGGGGACTCGTTTCTTGTAGTGGTCAATTCAGGATGACGTCGATT 1200  
Db 1141 CGGTGCTCTCAGGTAGGGGACTCGTTTCTTGTAGTGGTCAATTCAGGATGACGTCGATT 1200  
QY 1201 TGCCATGCCATGTCAAGGAAGCTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260  
Db 1201 TGCCATGCCATGTCAAGGAAGCTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260  
QY 1261 GGAATTTGAGCAGTGGCGCTGTATAGTACGATCGGCTCGGGCGCGGTGTCGGA 1320  
Db 1261 GGAATTTGAGCAGTGGCGCTGTATAGTACGATCGGCTCGGGCGCGGTGTCGGA 1320  
QY 1321 AGCAAAAAGGTGGTGGTTCGTTTACCGACAACATTTGATCCACACCTTGACATTTTCACCA 1380

Db 1321 AGCAAAAAGGTGGTGGTTCGTTTACCGACAACATTTGATCCCACTTGACATTTTCACCA 1380  
QY 1381 CCTCTTCCCGCCGAGAGCAAGCATTTGGCGGAAAAATCTATCTCGGCTACTATACAAG 1440  
Db 1381 CCTCTTCCCGCCGAGAGCAAGCATTTGGCGGAAAAATCTATCTCGGCTACTATACAAG 1440  
QY 1441 ATAGTCTTCGTATGGGACAAACCGTGGTGGCGGAACAAGGCTTCTCGGCGCTCTCCAA 1500  
Db 1441 ATAGTCTTCGTATGGGACAAACCGTGGTGGCGGAACAAGGCTTCTCGGCGCTCTCCAA 1500  
QY 1501 TCGAGCTGTGACCCCACTCTCATTTGGCAGAGATACCAAGCATCGAAGTCGATCGCAATGG 1560  
Db 1501 TCGAGCTGTGACCCCACTCTCATTTGGCAGAGATACCAAGCATCGAAGTCGATCGCAATGG 1560  
QY 1561 TCCATTACCTGTTTCATGGTTCGAGAGCCCGGAGGAAAGTGGTCCCAACAGTCCAAAGCAG 1620  
Db 1561 TCCATTACCTGTTTCATGGTTCGAGAGCCCGGAGGAAAGTGGTCCCAACAGTCCAAAGCAG 1620  
QY 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGAGCCCTACGAGAACGCGGGGCCCAA 1680  
Db 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGAGCCCTACGAGAACGCGGGGCCCAA 1680  
QY 1681 GTCCAGAGCCGCGCAACAGTCTCGAAATCGAGTGTGCGAAGCAGCAGTATTTCCAAGGA 1740  
Db 1681 GTCCAGAGCCGCGCAACAGTCTCGAAATCGAGTGTGCGAAGCAGCAGTATTTCCAAGGA 1740  
QY 1741 GTCCTGAGCGCGCTGATGGCTGAACGATCTCATCACACTGGGTTTCGCGCTCAAGACG 1800  
Db 1741 GTCCTGAGCGCGCTGATGGCTGAACGATCTCATCACACTGGGTTTCGCGCTCAAGACG 1800  
QY 1801 CCGTTCAAGTGTGTTTCATTTTGGAAACGAGACGCTTTTACGTTTGGAAAGGTTATG 1860  
Db 1801 CCGTTCAAGTGTGTTTCATTTTGGAAACGAGACGCTTTTACGTTTGGAAAGGTTATG 1860  
QY 1861 GAAGGGCCCATACGATCGGTCAACAGAGTGTCTGCAAGAGTTGTGGCTAGCCTGGTGCCA 1920  
Db 1861 GAAGGGCCCATACGATCGGTCAACAGAGTGTCTGCAAGAGTTGTGGCTAGCCTGGTGCCA 1920  
QY 1921 GCAGCATAG 1929  
Db 1921 GCAGCATAG 1929  
RESULT 2  
US-09-352-159-37  
; Sequence 37, Application US/09352159A  
; Patent No. 6211434  
; GENERAL INFORMATION:  
; APPLICANT: Duvick, Jonathan P.  
; APPLICANT: Gilliam, Jacob T.  
; APPLICANT: Maddox, Joyce R.  
; TITLE OF INVENTION: Amino Polyol Amine Oxidase  
; FILE REFERENCE: 1134  
; CURRENT APPLICATION NUMBER: US/09/352,159A  
; EARLIER FILING DATE: 1999-07-12  
; EARLIER APPLICATION NUMBER: 60/092,936  
; EARLIER FILING DATE: 1998-07-25  
; EARLIER APPLICATION NUMBER: 60/135,391  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 1929  
; TYPE: DNA  
; ORGANISM: Exophiala spinifera  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (739)...(811)  
; NAME/KEY: intron  
; LOCATION: (1134)...(1186)  
US-09-352-159-37

Query Match	94.7%;	Score 1827;	DB 4;	Length 1929;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1927;	Conservative	0;	Mismatches	2; Indels 0; Gaps
QY	1	ATGCGACTTGCACCGAGCTACATCAATCCCCAAACGTCGCCTCCCCAGCAGGATATTCC	60	
DB	1	ATGCGACTTGCACCGAGCTACATCAATCCCCAAACGTCGCCTCCCCAGCAGGATATTCC	60	
QY	61	CACATCGGCGTAGGCCCAAACGAGCGAGTATGTGACAAATAGCTGGACAGATTGGACAA	120	
DB	61	CACATCGGCGTAGGCCCAAACGAGCGAGTATGTGACAAATAGCTGGACAGATTGGACAA	120	
QY	121	GAGCTTTTGGCGGTGACAGACCAGCCTACGAGAAACAGTTGGCCACAGCATTCGCCCAAT	180	
DB	121	GAGCTTTTGGCGGTGACAGACCAGCCTACGAGAAACAGTTGGCCACAGCATTCGCCCAAT	180	
QY	181	CTGCGAGCTTGCCTTCTGCTCGAGTTGGAGCCTCTTCAAAACGAGCTACCAAGCTCAATTAC	240	
DB	181	CTGCGAGCTTGCCTTCTGCTCGAGTTGGAGCCTCTTCAAAACGAGCTACCAAGCTCAATTAC	240	
QY	241	TACATCGTCGACTACGCCCGGAGCAACTCACCGCAATTTGGAGATGGCTCAAGTCATACC	300	
DB	241	TACATCGTCGACTACGCCCGGAGCAACTCACCGCAATTTGGAGATGGCTCAAGTCATACC	300	
QY	301	TTTGGCCCTTGACAGGCTCCCTCTTTCGACGCTGGTGCCAGTACCGGCCCTTGGCTTCACTT	360	
DB	301	TTTGGCCCTTGACAGGCTCCCTCTTTCGACGCTGGTGCCAGTACCGGCCCTTGGCTTCACTT	360	
QY	361	GAAATACCTCTTTGAGGTTGATGCCAGCGGCGCTGGTGCCAGACACTCGACCCCAGACAAC	420	
DB	361	GAAATACCTCTTTGAGGTTGATGCCAGCGGCGCTGGTGCCAGACACTCGACCCCAGACAAC	420	
QY	421	GTTTGGGACGTGTACTGTTGGCGCGTGGCTTGGAGCGTGGAGACGSGACGCAAGATC	480	
DB	421	GTTTGGGACGTGTACTGTTGGCGCGTGGCTTGGAGCGTGGAGACGSGACGCAAGATC	480	
QY	481	CAGGCGCGCGGTCTGCTCTCGCTTCCTTGTAGGCGGATGGATCGTGTAGGGGGGAAAGACT	540	
DB	481	CAGGCGCGCGGTCTGCTCTCGCTTCCTTGTAGGCGGATGGATCGTGTAGGGGGGAAAGACT	540	
QY	541	CTGAGGCTACAAATCGGGTCCGGCAGGAGCACTATCAAGACCTTCGGCGCTTCGTGGATC	600	
DB	541	CTGAGGCTACAAATCGGGTCCGGCAGGAGCACTATCAAGACCTTCGGCGCTTCGTGGATC	600	
QY	601	AATGACAGCAACCAAAACGAAATATCCAGATTGTTTGAAGATTTCATTTGAGGCGCGAG	660	
DB	601	AATGACAGCAACCAAAACGAAATATCCAGATTGTTTGAAGATTTCATTTGAGGCGCGAG	660	
QY	661	CTCCAGAGACGACCGGAAATTCATTCATCAAGCACAAAGACGGTACAAACCACATACAGCT	720	
DB	661	CTCCAGAGACGACCGGAAATTCATTCATCAAGCACAAAGACGGTACAAACCACATACAGCT	720	
QY	721	CCTTATGTTGACTCCCGGTAAAGCAAAATCCCACTTTGTGATGAGACCTCTGTCCAGTGT	780	
DB	721	CCTTATGTTGACTCCCGGTAAAGCAAAATCCCACTTTGTGATGAGACCTCTGTCCAGTGT	780	
QY	781	AGAAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCACCTTGC	840	
DB	781	AGAAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTGCAAGTGCACCTTGC	840	
QY	841	GGAACTCTCTCCCGTATGTCCTCAGCTGATCAACAGATATAGCCTTGAAGACCCCAAGGC	900	
DB	841	GGAACTCTCTCCCGTATGTCCTCAGCTGATCAACAGATATAGCCTTGAAGACCCCAAGGC	900	
QY	901	GAGCCCTCAGGCGAAGCGCTCGACAGTGTGAGCTTCGCGCACTACTCTGTGAAAGAGCACT	960	
DB	901	GAGCCCTCAGGCGAAGCGCTCGACAGTGTGAGCTTCGCGCACTACTCTGTGAAAGAGCACT	960	
QY	961	AAACTTGCCTGCTGTTCTCAGCGTGGCAAAACAGATACACGCGCTCTGCTGGTGTGGA	1020	
DB	961	AAACTTGCCTGCTGTTCTCAGCGTGGCAAAACAGATACACGCGCTCTGCTGGTGTGGA	1020	

RESULT 3  
US-09-352-159-5  
; Sequence 5, Application US/09352159A  
; Patent No. 6211434  
; GENERAL INFORMATION:  
; APPLICANT: Duvick, Jonathan P.  
; APPLICANT: Gilliam, Jacob T.  
; APPLICANT: Maddox, Joyce R.

```
/ TITLE OF INVENTION: Amino Polyol Amine Oxidase
/ FILE REFERENCE: 1134
/ CURRENT APPLICATION NUMBER: US/09/352,159A
/ CURRENT FILING DATE: 1999-07-12
/ EARLIER APPLICATION NUMBER: 60/092,936
/ EARLIER FILING DATE: 1998-07-25
/ EARLIER APPLICATION NUMBER: 60/135,391
/ EARLIER FILING DATE: 1999-05-21
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 1389
/ TYPE: DNA
/ ORGANISM: Exophiala spinifera
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1386)
US-09-352-159-5

Query Match
Best Local Similarity 16.8%; Score 324; DB 4; Length 1389;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCCAACAGTCC 1614
Db 1015 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCCAACAGTCC 1074

QY 1615 AAGCAGGTACGACAAAAGTCTGTCGTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
Db 1675 AAGCAGGTACGACAAAAGTCTGTCGTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1134

QY 1675 GCCCAAGTCCCGAGCGGCCCAAGTGTCTGAAATCGAGTGTGCGAAGCAGTATTTC 1734
Db 1135 GCCCAAGTCCCGAGCGGCCCAAGTGTCTGAAATCGAGTGTGCGAAGCAGTATTTC 1194

QY 1735 CAAGAGTCCGAGCGCCCTCTATGGGTCGAAATCGAGTGTGCGGTCGAGAGTGTGCGGCTC 1794
Db 1195 CAAGAGTCCGAGCGCCCTCTATGGGTCGAAATCGAGTGTGCGGTCGAGAGTGTGCGGCTC 1254

QY 1795 AGAACCCGCTCAAGTGTCTTCAATTCGTTGGAACGAGACGCTTTAGTTTGGAAAGGG 1854
Db 1255 AGAACCCGCTCAAGTGTCTTCAATTCGTTGGAACGAGACGCTTTAGTTTGGAAAGGG 1314

QY 1855 TATATGGAAGGGCCATACGATCGGTCGAACGAGTGTGCGAAGTGTGCGTACGCTG 1914
Db 1315 TATATGGAAGGGCCATACGATCGGTCGAACGAGTGTGCGTACGCTG 1374

QY 1915 GTGCCAGCAGCATAG 1929
Db 1375 GTGCCAGCAGCATAG 1389

RESULT 4
US-09-352-168-5
/ Sequence 5, Application US/09352168A
/ Patent No. 6211435
/ GENERAL INFORMATION:
/ APPLICANT: Crusta, Oswald R.
/ APPLICANT: Duveick, Jonathan P.
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Gilliam, Jacob T.
/ APPLICANT: Maddox, Joyce R.
/ TITLE OF INVENTION: Amino Polyol Amine Oxidase
/ FILE REFERENCE: 0875
/ CURRENT APPLICATION NUMBER: US/09/352,168A
/ CURRENT FILING DATE: 1999-07-12
/ EARLIER APPLICATION NUMBER: 60/092,936
/ EARLIER FILING DATE: 1998-07-25
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
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/ LENGTH: 1389
/ TYPE: DNA
/ ORGANISM: Exophiala spinifera
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1386)
US-09-352-168-5

Query Match
Best Local Similarity 16.8%; Score 324; DB 4; Length 1389;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCCAACAGTCC 1614
Db 1015 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCCAACAGTCC 1074

QY 1615 AAGCAGGTACGACAAAAGTCTGTCGTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
Db 1075 AAGCAGGTACGACAAAAGTCTGTCGTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1134

QY 1675 GCCCAAGTCCCGAGCGGCCCAAGTGTCTGAAATCGAGTGTGCGGTCGAGAGTGTGCGGCTC 1734
Db 1135 GCCCAAGTCCCGAGCGGCCCAAGTGTCTGAAATCGAGTGTGCGGTCGAGAGTGTGCGGCTC 1194

QY 1735 CAAGAGTCCGAGCGCCCTCTATGGGTCGAAATCGAGTGTGCGGTCGAGAGTGTGCGGCTC 1794
Db 1195 CAAGAGTCCGAGCGCCCTCTATGGGTCGAAATCGAGTGTGCGGTCGAGAGTGTGCGGCTC 1254

QY 1795 AGAACCCGCTCAAGTGTCTTCAATTCGTTGGAACGAGACGCTTTAGTTTGGAAAGGG 1854
Db 1255 AGAACCCGCTCAAGTGTCTTCAATTCGTTGGAACGAGACGCTTTAGTTTGGAAAGGG 1314

QY 1855 TATATGGAAGGGCCATACGATCGGTCGAACGAGTGTGCGAAGTGTGCGTACGCTG 1914
Db 1315 TATATGGAAGGGCCATACGATCGGTCGAACGAGTGTGCGTACGCTG 1374

QY 1915 GTGCCAGCAGCATAG 1929
Db 1375 GTGCCAGCAGCATAG 1389

RESULT 5
US-09-352-159-10
/ Sequence 10, Application US/09352159A
/ Patent No. 6211434
/ GENERAL INFORMATION:
/ APPLICANT: Duveick, Jonathan P.
/ APPLICANT: Gilliam, Jacob T.
/ APPLICANT: Maddox, Joyce R.
/ TITLE OF INVENTION: Amino Polyol Amine Oxidase
/ FILE REFERENCE: 1134
/ CURRENT APPLICATION NUMBER: US/09/352,159A
/ CURRENT FILING DATE: 1999-07-12
/ EARLIER APPLICATION NUMBER: 60/092,936
/ EARLIER FILING DATE: 1998-07-25
/ EARLIER APPLICATION NUMBER: 60/135,391
/ EARLIER FILING DATE: 1999-05-21
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10
/ LENGTH: 1392
/ TYPE: DNA
/ ORGANISM: Exophiala spinifera
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1389)
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(3)
/ OTHER INFORMATION: Extra lysine in K:trAPAQ
US-09-352-159-10

Query Match
Best Local Similarity 16.8%; Score 324; DB 4; Length 1392;
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Best Local Similarity	99.7%;	Pred. No. 3.3e-159;			
Matches 374;	Conservative	0;	Mismatches 1;	Indels	0; Gaps 0;
QY	1555	CAATGGTCCATTACCTGTTTTCATGTCGGAGACCCGGGACGGAAGTGTCCTCCCAACAGTCCT	1614		
Db	1018	CAATGGTCCATTACCTGTTTTCATGTCGGAGACCCGGGACGGAAGTGTCCTCCCAACAGTCCT	1077		
QY	1615	AGCAGGTACGACAAAGCTGTCCTGGAGCCAACTCCGGCGACGCTTACGAGAACGCCGGG	1674		
Db	1078	AGCAGGTACGACAAAGCTGTCCTGGAGCCAACTCCGGCGACGCTTACGAGAACGCCGGG	1137		
QY	1675	GCCAAAGTCCCAAGACCCGGCCAAAGTGTCTCGAAATCGAGTGTCTCGAAGCAGCAGTATTTC	1734		
Db	1138	GCCAAAGTCCCAAGACCCGGCCAAAGTGTCTCGAAATCGAGTGTCTCGAAGCAGCAGTATTTC	1197		
QY	1735	CAAGGAGCTCCAGAGCCGCGTCTATGGGCTGAACGATCTCATCACTGGTGTGGCGGTC	1794		
Db	1198	CAAGGAGCTCCAGAGCCGCGTCTATGGGCTGAACGATCTCATCACTGGTGTGGCGGTC	1257		
QY	1795	AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAAACGGAGACGCTTTTAGTGTGGAAAGG	1854		
Db	1258	AGAACGCCGTTCAAGAGTGTTCATTTCTGTTGGAAACGGAGACGCTTTTAGTGTGGAAAGG	1317		
QY	1855	TATATGAAGGGCCATACGATCGGGTCAACGAGGTCTCGAAGCTGTGGCTAGCCTG	1914		
Db	1318	TATATGAAGGGCCATACGATCGGGTCAACGAGGTCTCGAAGCTGTGGCTAGCCTG	1377		
QY	1915	GTGCCAGCAGCATAG	1929		
Db	1378	GTSCCAGCAGCATAG	1392		

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RESULT 6
US-09-352-168-10
; Sequence 10, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1389)
; NAME/KEY: misc_feature
; LOCATION: (1)...(3)
; OTHER INFORMATION: Extra lysine in K:trapa0
US-09-352-168-10

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7	RESULT
US-09-35	: Sequen
:	: Patent
:	: GENERA
:	: APPLI
:	: APPLI
:	: TITLE
:	: FILE
:	: CURRE
:	: CURRE
:	: EARLI
:	: EARLI
:	: EARLI
:	: EARLI
:	: NUMBE
:	: SOFTW
:	: SEQ ID
:	: LENG
:	: TYPE
:	: ORGA
:	: FEAT
:	: NAME
:	: NAME
:	: LOCAL
:	: NAME
:	: LOCA
:	: NAME
:	: LOCA
US-09-35	

	Query Match	16.8%;	Score 324;	DB 4;	Length 1442;	
	Best Local Similarity	99.7%;	Pred. No. 3.3e-159;			
	Matches 374;	Conservative	0;	Mismatches 1;	Indels	0; Gaps 0;
QY	1555	CAATGGTCCATTACCTGTTTCATGTCGGAGACCGCGGACGGAAGTGGTCCCAACAGTC	1614			
DB	1068	CAATGGTCCATTACCTGTTTCATGTCGGAGACCGCGGACGGAAGTGGTCCCAACAGTC	1127			
QY	1615	AAGCAGGTACGACAAAGTCTCTGTGGACCAACTCCGCGCAGCGCTACGAGAACGCCGG	1674			
DB	1128	AAGCAGGTACGACAAAGTCTCTGTGGACCAACTCCGCGCAGCGCTACGAGAACGCCGG	1187			
QY	1675	GCCCAAGTCCCGAGCGCGGCCAACGTGCTCGAAATCGAGTGGTCCGAAGCAGCAGTATTTTC	1734			
DB	1188	GCCCAAGTCCCGAGCGCGGCCAACGTGCTCGAAATCGAGTGGTCCGAAGCAGCAGTATTTTC	1247			
QY	1735	CAAGGAGCTCCGAGCGCGGCTCTATGGCTGGAACGATCTCATCACACTGGGTTCGGCGGCTC	1794			

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Db 1248 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGTC 1307
QY 1795 AGAAGCGCGTTCAAGTGTGTTCACTTGGTTGGAACGAGACGCTCTTTAGTTGGAAAGG 1854
Db 1308 AGAAGCGCGTTCAAGAGTGTTCATTTGGTTGGAACGAGACGCTCTTTAGTTGGAAAGG 1367
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTGTGGCTAGCCTG 1914
Db 1368 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTGTGGCTAGCCTG 1427
QY 1915 GTGCCAGCAGCATAG 1929
Db 1428 GTGCCAGCAGCATAG 1442

RESULT 8
US-09-352-168-7
; Sequence 7, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; EARLIER FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(646)
; NAME/KEY: intron
; LOCATION: (647)...(699)
; NAME/KEY: CDS
; LOCATION: (700)...(1439)
US-09-352-168-7

Query Match 16.8%; Score 324; DB 4; Length 1442;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGGTCCGAGACCCGGGACGGAGTGGTCCCAACAGTCC 1614
Db 1068 CAATGGTCCATTACCTGTTTCATGGTCCGAGACCCGGGACGGAGTGGTCCCAACAGTCC 1127
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCACTCCGCGCAGCTTACGAGAACGCCGG 1674
Db 1128 AAGCAGGTACGACAAAAGTCTGTCTGGGACCACTCCGCGCAGCTTACGAGAACGCCGG 1187
QY 1675 GCCCAAGTCCCAGACCGCGGCAACGTCGCTCGAAATCGAGTGGTCGAGCAGCATTTTC 1734
Db 1188 GCCCAAGTCCCAGACCGCGGCAACGTCGCTCGAAATCGAGTGGTCGAGCAGCATTTTC 1247
QY 1735 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGTC 1794
Db 1248 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGTC 1307
QY 1795 AGAAGCGCGTTCAAGTGTGTTCACTTGGTTGGAACGAGACGCTCTTTAGTTGGAAAGG 1854
Db 1308 AGAAGCGCGTTCAAGAGTGTTCATTTGGTTGGAACGAGACGCTCTTTAGTTGGAAAGG 1367
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTGTGGCTAGCCTG 1914
Db 1368 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTGTGGCTAGCCTG 1427
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Db 1368 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTGTGGCTAGCCTG 1427
QY 1915 GTGCCAGCAGCATAG 1929
Db 1428 GTGCCAGCAGCATAG 1442

RESULT 9
US-09-352-159-20
; Sequence 20, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; EARLIER FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of K:trPAO translational
; OTHER INFORMATION: fusion with barley alpha amylase signal sequence.
; OTHER INFORMATION: for expression and secretion of the mature trPAO
; OTHER INFORMATION: in maize. Nucleotides 1-72, barley alpha amylase
; OTHER INFORMATION: signal sequence, nucleotides 73-75, added lysine
; OTHER INFORMATION: residue; nucleotides 76-1464, trPAO cDNA.
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(72)
; OTHER INFORMATION: Barley alpha amylase signal sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (73)...(1464)
; OTHER INFORMATION: K:trPAOcDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1461)
; NAME/KEY: misc_feature
; LOCATION: (73)...(75)
; OTHER INFORMATION: Added lysine residue
US-09-352-159-20

Query Match 16.8%; Score 324; DB 4; Length 1464;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGGTCCGAGACCCGGGACGGAGTGGTCCCAACAGTCC 1614
Db 1090 CAATGGTCCATTACCTGTTTCATGGTCCGAGACCCGGGACGGAGTGGTCCCAACAGTCC 1149
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCACTCCGCGCAGCTTACGAGAACGCCGG 1674
Db 1150 AAGCAGGTACGACAAAAGTCTGTCTGGGACCACTCCGCGCAGCTTACGAGAACGCCGG 1209
QY 1675 GCCCAAGTCCCAGACCGCGGCAACGTCGCTCGAAATCGAGTGGTCGAGCAGCATTTTC 1734
Db 1210 GCCCAAGTCCCAGACCGCGGCAACGTCGCTCGAAATCGAGTGGTCGAGCAGCATTTTC 1269
QY 1735 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGTC 1794
Db 1270 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGTC 1329
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QY 1795 AGAACCCCGTTCAAGTGTTTCATTTCTGTTGGAACGGAGACGCTTTTAGTTTGGAAAGG 1854
|||||
Db 1330 AGAACCCCGTTCAAGAGTGTTCATTTCTGTTGGAACGGAGACGCTTTTAGTTTGGAAAGG 1389
|||||
QY 1855 TATATGGAAGGGCCATAGTCGGGTCAACGAGTGTGTGAGAAGTTGTGGCTAGCCCTG 1914
|||||
Db 1390 TATATGGAAGGGCCATAGTCGGGTCAACGAGTGTGTGAGAAGTTGTGGCTAGCCCTG 1449
|||||
QY 1915 GTGCCAGCAGCATAG 1929
|||||
Db 1450 GTGCCAGCAGCATAG 1464

RESULT 10
US-09-352-168-20
; Sequence 20, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352.168A
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(72)
; OTHER INFORMATION: Barley Alpha Amylase signal sequence.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (73)...(1464)
; OTHER INFORMATION: K:trPAOcdNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1461)
; OTHER INFORMATION: Nucleotide sequence of K:trPAO translational
; OTHER INFORMATION: fusion with barley alpha amylase signal sequence,
; OTHER INFORMATION: for expression and secretion of the mature trPAO
; OTHER INFORMATION: in maize. Nucleotides 1-72, barley alpha amylase
; OTHER INFORMATION: signal sequence, nucleotides 73-75, added lysine
; OTHER INFORMATION: residue; nucleotides 76 -1464 , trPAO cdna.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (73)...(75)
; OTHER INFORMATION: Added lysine residue
US-09-352-168-20

Query Match 16.8%; Score 324; DB 4; Length 1464;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1090 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGAGCGGAAGTGGTCCCAACAGTCC 1149
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QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAAACGCCGG 1674
|||||
Db 1150 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAAACGCCGG 1209
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QY 1675 GCCCAAGTCCAGAGCCGCCAAGCTGCTGAAATCGAGTGGTCTGGAAGGAGACGAGTATTC 1734
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Db 1210 GCCCAAGTCCAGAGCCGCCAAGCTGCTGAAATCGAGTGGTCTGGAAGCAGCAGTATTC 1269
QY 1735 CAAGGAGCTCGAGCCGCCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
|||||
Db 1270 CAAGGAGCTCCGAGCGCCGCTCTATGGGCTGAAGGATCTCATCACACTGGGTTCGGCGCTC 1329
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QY 1795 AGAACCCCGTTCAAGTGTTTCATTTCTGTTGGAACGGAGACGCTTTTAGTTTGGAAAGG 1854
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Db 1330 AGAACCCCGTTCAAGTGTTTCATTTCTGTTGGAACGGAGACGCTTTTAGTTTGGAAAGG 1389
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QY 1855 TATATGGAAGGGCCATAGTCGGGTCAACGAGTGTGTGAGAAGTTGTGGCTAGCCCTG 1914
|||||
Db 1390 TATATGGAAGGGCCATAGTCGGGTCAACGAGTGTGTGAGAAGTTGTGGCTAGCCCTG 1449
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QY 1915 GTGCCAGCAGCATAG 1929
|||||
Db 1450 GTGCCAGCAGCATAG 1464

RESULT 11
US-09-352-159-16
; Sequence 16, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(267)
; OTHER INFORMATION: Yeast alpha mating factor secretion signal.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1662)
US-09-352-159-16

Query Match 16.8%; Score 324; DB 4; Length 1673;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGAGCGGAAGTGGTCCCAACAGTCC 1614
|||||
Db 1291 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGAGCGGAAGTGGTCCCAACAGTCC 1350
|||||
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAAACGCCGG 1674
|||||
Db 1351 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAAACGCCGG 1410
|||||
QY 1675 GCCCAAGTCCAGAGCCGCCAAGCTGCTGAAATCGAGTGGTCTGGAAGGAGACGAGTATTC 1734
|||||
Db 1411 GCCCAAGTCCAGAGCCGCCAAGCTGCTGAAATCGAGTGGTCTGGAAGGAGACGAGTATTC 1470
|||||
QY 1735 CAAGGAGCTCCGAGCGCCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
|||||
Db 1471 CAAGGAGCTCCGAGCGCCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1530
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QY 1795 AGAACCCCGTTCAAGTGTTTCATTTCTGTTGGAAGGAGACGCTTTTAGTTTGGAAAGG 1854
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Db	1531	AGAACGCCGTTCAAGAGTGTTTCATTTCTGTTGGAAACGAGACGCTCTTTAGTTTGGAAAGG	1590
Qy	1855	TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG	1914
Db	1591	TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG	1650
Qy	1915	GTGCCAGCAGCATAG	1929
Db	1651	GTGCCAGCAGCATAG	1665
RESULT 12			
US-09-352-168-16			
Sequence 16, Application US/09352168A			
Patent No. 6211435			
GENERAL INFORMATION:			
APPLICANT: Crasta, Oswald R.			
APPLICANT: Duwick, Jonathan P.			
APPLICANT: Folkerts, Otto			
APPLICANT: Gilliam, Jacob T.			
APPLICANT: Madcox, Joyce R.			
TITLE OF INVENTION: Amino Polyol Amine Oxidase			
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use			
FILE REFERENCE: 0875			
CURRENT APPLICATION NUMBER: US/09/352,168A			
CURRENT FILING DATE: 1999-07-12			
EARLIER APPLICATION NUMBER: 60/092,936			
EARLIER FILING DATE: 1998-07-25			
NUMBER OF SEQ ID NOS: 33			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 16			
LENGTH: 1673			
TYPE: DNA			
ORGANISM: Exophiala spinifera			
FEATURE:			
NAME/KEY: sig_peptide			
LOCATION: (1)...(267)			
OTHER INFORMATION: yeast alpha mating factor secretion signal.			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1)...(1662)			
US-09-352-168-16			
Query Match	16.8%;	Score 324; DB 4; Length 1673;	
Best Local Similarity	99.7%;	Pred. No. 3.3e-159;	
Matches	374; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1555	CAATGGTCCATTACCTGTTTCATGTCGGAGACCGCGGACGGAAGTGTGCCACAGTCC	1614
Db	1291	CAATGGTCCATTACCTGTTTCATGTCGGAGACCGCGGACGGAAGTGTGCCACAGTCC	1350
Qy	1615	RAGCAGGTACGACAAAGTCTGCTGGACCAACTCCGCGAGCTACGAAACGCCGGG	1674
Db	1351	RAGCAGGTACGACAAAGTCTGCTGGACCAACTCCGCGAGCTACGAAACGCCGGG	1410
Qy	1675	GCCCAAGTCCGACAGCGCGCAACGTGCTGAAATCGAGTGGTGAACGACGAGTATTC	1734
Db	1411	GCCCAAGTCCGACAGCGCGCAACGTGCTGAAATCGAGTGGTGAACGACGAGTATTC	1470
Qy	1735	CAAGGAGTCCGAGCGCGTCTATGGGTGAACGATCATCACACTGGGTTCGGCGCTC	1794
Db	1471	CAAGGAGTCCGAGCGCGTCTATGGGTGAACGATCATCACACTGGGTTCGGCGCTC	1530
Qy	1795	AGAACCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGAGCTCTTTAGTTGGAAGG	1854
Db	1531	AGAACCCGTTCAAGAGTGTTCATTTCTGTTGGAACGGAGAGCTCTTTAGTTGGAAGG	1590
Qy	1855	TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG	1914
Db	1591	TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG	1650
Qy	1915	GTGCCAGCAGCATAG	1929

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; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1800)
US-09-352-168-22

Query Match      16.8%; Score 324; DB 4; Length 1803;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1615 AAGCAGGTACGACAAAGTCTGCTGGGACCAACTCCCGCGAGCCTACGAGAACGCCGGG 1674
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QY 1675 GCCAAGTCCGAGCGCGCCAACTGCTCGAATCGAGTGTGCGAACGACGAGTATTTTC 1734
Db 1549 GCCAAGTCCGAGCGCGCCAACTGCTCGAATCGAGTGTGCGAACGACGAGTATTTTC 1608
QY 1735 CAAGGAGCTCCGAGCGCCGCTATGGCTGAACGATCTCATCACACTCGGTTCCGCGCTC 1794
Db 1609 CAAGGAGCTCCGAGCGCCGCTATGGCTGAACGATCTCATCACACTCGGTTCCGCGCTC 1668
QY 1795 AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGGG 1854
Db 1669 AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGGG 1728
QY 1855 TATATGGAAGGGCCATACGATCGGTCACACGAGTGTGCGAAGTGTGCGTAGCCTG 1914
Db 1729 TATATGGAAGGGCCATACGATCGGTCACACGAGTGTGCGAAGTGTGCGTAGCCTG 1788
QY 1915 GTGCCAGCAGCATAG 1929
Db 1789 GTGCCAGCAGCATAG 1803

RESULT 15
US-09-352-159-39
; Sequence 39, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gillingham, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 1930
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; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: intron
; LOCATION: (739)....(811)
; NAME/KEY: intron
; LOCATION: (1134)....(1187)
; NAME/KEY: misc feature
; LOCATION: (648)....(648)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-159-39

Query Match      16.8%; Score 324; DB 4; Length 1930;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGACCGGAAGTGTGCCACACAGTCC 1614
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QY 1615 AAGCAGGTACGACAAAGTCTGCTGGGACCAACTCCCGCGAGCCTACGAGAACGCCGGG 1674
Db 1616 AAGCAGGTACGACAAAGTCTGCTGGGACCAACTCCCGCGAGCCTACGAGAACGCCGGG 1675
QY 1675 GCCAAGTCCGAGCGCGCCAACTGCTCGAATCGAGTGTGCGAACGACGAGTATTTTC 1734
Db 1676 GCCAAGTCCGAGCGCGCCAACTGCTCGAATCGAGTGTGCGAACGACGAGTATTTTC 1735
QY 1735 CAAGGAGCTCCGAGCGCCGCTATGGCTGAACGATCTCATCACACTCGGTTCCGCGCTC 1794
Db 1736 CAAGGAGCTCCGAGCGCCGCTATGGCTGAACGATCTCATCACACTCGGTTCCGCGCTC 1795
QY 1795 AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGGG 1854
Db 1796 AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGGG 1855
QY 1855 TATATGGAAGGGCCATACGATCGGTCACACGAGTGTGCGAAGTGTGCGTAGCCTG 1914
Db 1856 TATATGGAAGGGCCATACGATCGGTCACACGAGTGTGCGAAGTGTGCGTAGCCTG 1915
QY 1915 GTGCCAGCAGCATAG 1929
Db 1916 GTGCCAGCAGCATAG 1930

Search completed: November 12, 2002, 07:55:23
Job time : 87 secs
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OM nucleic - nucleic search, using sw model

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(without alignments)  
8346.111 Million cell updates/sec

Title: US-09-771-045A-35

Perfect score: 1929

Sequence: 1 atggcaattgcaccagagcta.....gcctggtgcagcagcatag 1929

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

Word size : 0

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	19	1.0	222	10	US-09-833-263-887
3	19	1.0	228	10	US-09-922-217-939
4	19	1.0	228	10	US-09-833-263-939
5	17	0.9	239	10	US-09-878-574-10314
6	17	0.9	261	10	US-09-878-574-7447
7	17	0.9	264	10	US-09-923-876-1462
8	17	0.9	433	10	US-09-960-352-7464
9	17	0.9	443	10	US-09-960-352-4610
10	17	0.9	476	10	US-09-864-761-2462
11	17	0.9	597	10	US-09-864-761-7247
12	17	0.9	610	10	US-09-864-761-19193
13	17	0.9	826	10	US-09-770-445-714
14	17	0.9	880	9	US-09-938-842A-4623
15	17	0.9	1657	10	US-09-925-301-134
16	17	0.9	1884	9	US-09-938-842A-905
17	17	0.9	2247	10	US-09-974-300-170
18	17	0.9	4719	9	US-09-808-602-57
19	17	0.9	5502	9	US-09-808-602-3

20	16	0.8	77	10	US-09-844-508-24	Sequence 24, Appl
21	16	0.8	83	9	US-09-942-087A-26	Sequence 26, Appl
22	16	0.8	83	10	US-09-779-233-14	Sequence 14, Appl
23	16	0.8	203	10	US-09-960-352-12039	Sequence 12039, A
24	16	0.8	235	10	US-09-923-876-3532	Sequence 3532, Ap
25	16	0.8	241	10	US-09-960-352-12494	Sequence 12494, A
26	16	0.8	243	10	US-09-960-352-12759	Sequence 12759, A
27	16	0.8	248	10	US-09-923-876-3057	Sequence 3057, Ap
28	16	0.8	253	10	US-09-960-352-5418	Sequence 5418, Ap
29	16	0.8	263	10	US-09-923-876-1830	Sequence 1830, Ap
30	16	0.8	269	10	US-09-923-876-515	Sequence 515, App
31	16	0.8	331	10	US-09-878-574-2802	Sequence 2802, Ap
32	16	0.8	340	10	US-09-770-791-845	Sequence 845, App
33	16	0.8	348	10	US-09-783-590-10561	Sequence 10561, A
34	16	0.8	353	10	US-09-770-791-666	Sequence 666, App
35	16	0.8	380	10	US-09-960-352-14899	Sequence 14899, A
36	16	0.8	390	10	US-09-770-791-18	Sequence 18, Appl
37	16	0.8	391	10	US-09-604-287A-227	Sequence 227, App
38	16	0.8	391	10	US-09-339-338-227	Sequence 227, App
39	16	0.8	391	12	US-10-007-805-227	Sequence 227, App
40	16	0.8	399	10	US-09-864-761-29869	Sequence 29869, A
41	16	0.8	412	10	US-09-960-352-1982	Sequence 1982, Ap
42	16	0.8	417	10	US-09-960-352-9410	Sequence 9410, Ap
43	16	0.8	418	10	US-09-783-590-2288	Sequence 2288, Ap
44	16	0.8	418	10	US-09-960-352-9138	Sequence 9138, Ap
45	16	0.8	422	10	US-09-867-701-5519	Sequence 5519, Ap

#### ALIGNMENTS

RESULT 1  
US-09-922-217-887  
; Sequence 887, Application US/09922217  
; Patent No. US20020076414A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Smith, Carole Lynn  
; APPLICANT: King, Gordon E.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Clapper, Jonathan D.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.471C13  
; CURRENT APPLICATION NUMBER: US/09/922,217  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 1124  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 887  
; LENGTH: 222  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-922-217-887

Query Match 1.0%; Score 19; DB 10; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1686  
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Db 170 CGCCGGGGCCCAAGTCCCA 188

RESULT 2  
US-09-833-263-887  
; Sequence 887, Application US/09833263

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; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 887
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-833-263-939

Query Match      1.0%; Score 19; DB 10; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1686
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Db 170 CGCCGGGGCCCAAGTCCCA 188

RESULT 3
US-09-922-217-939
; Sequence 939, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 939
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-922-217-939

Query Match      1.0%; Score 19; DB 10; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1686
      |||||
Db 170 CGCCGGGGCCCAAGTCCCA 188

RESULT 4
US-09-833-263-939
; Sequence 939, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 887
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-833-263-939

Query Match      1.0%; Score 19; DB 10; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1686
      |||||
Db 170 CGCCGGGGCCCAAGTCCCA 188

RESULT 5
US-09-878-574-10314
; Sequence 10314, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 10314
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701103537H1
; US-09-878-574-10314

Query Match      0.9%; Score 17; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CTCAAATTACTACATCGT 248
      |||||
Db 37 CTCAAATTACTACATCGT 53

RESULT 6
US-09-878-574-7447
; Sequence 7447, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
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; SEQ ID NO 7447
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701099887H1
US-09-878-574-7447

Query Match          0.9%; Score 17; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CTCGAATTACTACATCGT 248
      |||||
Db 35 CTCGAATTACTACATCGT 51

RESULT 7
US-09-923-876-1462/c
; Sequence 1462, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalagudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 1462
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700158849H1
; NAME/KEY: unsure
; LOCATION: 250, 254, 261, 263
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-1462

Query Match          0.9%; Score 17; DB 10; Length 264;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1073 GGTCCTCAGTAATATGCT 1089
      |||||
Db 75 GGTCCTCAGTAATATGCT 59

RESULT 8
US-09-960-352-7464
; Sequence 7464, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7464
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 32-LIB3058-049-Q1-K1-H7
US-09-960-352-7464

Query Match          0.9%; Score 17; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1625 GACAAAGAGTCTGCTGG 1641
      |||||
Db 136 GACAAAGAGTCTGCTGG 152

RESULT 9
US-09-960-352-4610/c
; Sequence 4610, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4610
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB3058-021-Q1-K1-E7
US-09-960-352-4610

Query Match          0.9%; Score 17; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 636 TGAAGATTTTCATTGG 652
      |||||
Db 351 TGAAGATTTTCATTGG 335

RESULT 10
US-09-864-761-2462
; Sequence 2462, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2462
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL080243.21
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 28
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 70
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 25
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 55
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.3
; US-09-864-761-2462
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Query Match 0.9%; Score 17; DB 10; Length 476;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 864 AGCTGATCGAAGAGTAT 880
Db 24 AGCTGATCGAAGAGTAT 40
|||||
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RESULT 11
US-09-864-761-7247/c
; Sequence 7247, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 7247
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC015649.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; US-09-864-761-7247
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Query Match 0.9%; Score 17; DB 10; Length 597;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1207 GCCATGTCAAAGAACT 1223
Db 375 GCCATGTCAAAGAACT 359
|||||
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```
RESULT 12
US-09-864-761-19193
; Sequence 19193, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
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; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-27  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 19193  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL080243.21  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.7  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 28  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 70  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 16  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 25  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 55  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.3  
; OTHER INFORMATION: EST\_HUMAN HIT: B6795542.1, EVALUE 0.00e+00  
; OTHER INFORMATION: NT HIT: g111424380, EVALUE 0.00e+00  
; OTHER INFORMATION: SWISSPROT HIT: P29314, EVALUE 8.00e-90  
US-09-864-761-19193

Query Match 0.9%; Score 17; DB 10; Length 610;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 864 AGCTGATCGAAGATAT 880  
|||||

DB 114 AGCTGATCGAAGATAT 130

RESULT 13  
US-09-770-445-714  
; Sequence 714, Application US/09770445  
; Patent No. US20020023281A1  
; GENERAL INFORMATION:  
; APPLICANT: Gorlach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krickler, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2023US (PARA-012PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,445  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/178,472  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 714  
; LENGTH: 826  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-445-714

Query Match 0.9%; Score 17; DB 10; Length 826;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 AGTCACTGACTCCACTT 804  
|||||

DB 739 AGTCACTGACTCCACTT 755

RESULT 14  
US-09-938-842A-4623/C  
; Sequence 4623, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SCRI1300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 4623  
; LENGTH: 880  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-4623

Query Match 0.9%; Score 17; DB 9; Length 880;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 751 CCACCTTGTGTGATGAGAC 767  
|||||

DB 47 CCACCTTGTGTGATGAGAC 31

```
RESULT 15
US-09-925-301-134/C
; Sequence 134, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 134
; LENGTH: 1657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-134

Query Match          0.9%; Score 17; DB 10; Length 1657;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 CTCCTTATGGTGACTCC 735
    |||
Db 1085 CTCCTTATGGTGACTCC 1069

Search completed: November 12, 2002, 07:56:54
JOB time : 85 secs
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